

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 05:46:47 ; Search time 39.2079 Seconds

(without alignments)
69.968 Million cell updates/sec

Title: US-10-541-343-2

Perfect score: 31

Sequence: 1 FSRVYR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	ADQ90196	Adq90196 FSRVYR 6
2	31	100.0	10	ADQ90198	Adq90198 MNTF 10 m
3	31	100.0	11	ADQ90199	Adq90199 MNTF 11 m
4	31	100.0	13	ADQ90200	Adq90200 MNTF 13 m
5	31	100.0	21	ADQ90201	Adq90201 MNTF 21 m
6	31	100.0	21	AEAI7675	Aeai7675 Motoneuro
7	31	100.0	33	AAW59046	AAW59046 Human MNT
8	31	100.0	33	AAO29914	AAO29914 Human mot
9	31	100.0	33	ADQ90195	Adq90195 MNTF1-F6
10	31	100.0	81	AAU57756	AAU57756 Propionib
11	31	100.0	81	ABM54275	ABM54275 Propionib
12	31	100.0	112	AAU57258	AAU57258 Propionib
13	31	100.0	112	ABM53777	ABM53777 Propionib
14	31	100.0	174	ABM64633	ABM64633 Propionib
15	31	100.0	357	AAV35559	AAV35559 Chlamydia
16	31	100.0	357	ABR90579	ABR90579 Chlamydia
17	31	100.0	357	ABU27032	ABU27032 Protein e
18	31	100.0	357	ABU27032	ABU27032 Protein e
19	31	100.0	463	ADSA4828	ADSA4828 Bacterial
20	31	100.0	466	AAE23630	AAE23630 Escherich
21	31	100.0	474	AAU34677	AAU34677 E. coli c
22	31	100.0	474	ADSA5088	ADSA5088 Bacterial
23	31	100.0	509	ABO74595	ABO74595 Pseudomon

24	31	100.0	1225	4	ABG24444	Abg24444 Novel hum
25	31	100.0	1258	4	ABG24819	Abg24819 Novel hum
26	28	90.3	58	4	AAU60688	AAU60688 Propionib
27	28	90.3	58	6	ABM57207	ABM57207 Propionib
28	28	90.3	85	2	AAV12203	AAV12203 Human 5'
29	28	90.3	90	6	ABR40679	ABR40679 Oryza sat
30	28	90.3	132	2	ABR40677	ABR40677 Oryza sat
31	28	90.3	139	2	AAW67901	AAW67901 Human sec
32	28	90.3	145	6	ADB06538	ADB06538 Altiococ
33	28	90.3	172	6	ADB06540	ADB06540 Altiococ
34	28	90.3	174	2	AAW67842	AAW67842 Human sec
35	28	90.3	174	6	ADY14896	ADY14896 PRO polyp
36	28	90.3	174	10	AEF69875	AEF69875 Microsate
37	28	90.3	243	37	AEAI7517	AEAI7517 Thale cre
38	28	90.3	244	6	ABR40670	ABR40670 Zea mays
39	28	90.3	256	8	ADX91903	ADX91903 Plant ful
40	28	90.3	301	4	ABG07163	ABG07163 Novel hum
41	28	90.3	301	9	AEAI7523	AEAI7523 Thale cre
42	28	90.3	301	9	AEAI7522	AEAI7522 Thale cre
43	28	90.3	499	4	ABG27724	ABG27724 Novel hum
44	28	90.3	520	4	ABG29681	ABG29681 Novel hum
45	28	90.3	661	8	ADN18185	ADN18185 Bacterial
46	28	90.3	847	4	ABG04036	ABG04036 Novel hum
47	28	90.3	1206	6	ABP76771	ABP76771 N. gonorr
48	28	90.3	1206	6	ABP76681	ABP76681 N. gonorr
49	28	90.3	1778	7	ABG69413	ABG69413 Pseudomon
50	28	90.3	2151	5	ABR78221	ABR78221 Alpha1C s
51	28	87.1	51	8	ADS07116	ADS07116 Stephyloc
52	27	87.1	59	4	AAU14729	AAU14729 Novel bon
53	27	87.1	182	7	ABM89390	ABM89390 Rice abio
54	27	87.1	198	7	ABO83305	ABO83305 Pseudomon
55	27	87.1	208	3	AAG22027	AAG22027 Arabidops
56	27	87.1	209	3	AAG46509	AAG46509 Arabidops
57	27	87.1	209	3	AAG35926	AAG35926 Arabidops
58	27	87.1	209	3	AAG24637	AAG24637 Arabidops
59	27	87.1	209	8	ADT56063	ADT56063 Plant pol
60	27	87.1	217	3	AAG24636	AAG24636 Arabidops
61	27	87.1	217	3	AAG46508	AAG46508 Arabidops
62	27	87.1	218	3	AAG22026	AAG22026 Arabidops
63	27	87.1	220	3	ABAB3764	ABAB3764 Human can
64	27	87.1	272	8	ADX90400	ADX90400 Plant ful
65	27	87.1	284	3	AAG05948	AAG05948 Arabidops
66	27	87.1	290	3	AAG05372	AAG05372 Arabidops
67	27	87.1	313	3	AAG05947	AAG05947 Arabidops
68	27	87.1	341	2	AAW54385	AAW54385 Actinomad
69	27	87.1	354	6	ABU38270	ABU38270 Pseudomon
70	27	87.1	354	6	ABU41318	ABU41318 Protein e
71	27	87.1	364	7	ABO71135	ABO71135 Pseudomon
72	27	87.1	367	7	ABO67510	ABO67510 Klebsiell
73	27	87.1	409	8	ADSA1920	ADSA1920 Bacterial
74	27	87.1	410	8	ABAB96590	ABAB96590 Putative
75	27	87.1	410	8	ADN18631	ADN18631 Bacterial
76	27	87.1	410	8	ADSA43194	ADSA43194 Bacterial
77	27	87.1	414	7	ADBE80738	ADBE80738 Microsate
78	27	87.1	428	7	ADBE80739	ADBE80739 Microsate
79	27	87.1	445	3	ABAB16689	ABAB16689 Bacteriop
80	27	87.1	456	8	ADS25032	ADS25032 Bacterial
81	27	87.1	456	5	AAE23631	AAE23631 Escherich
82	27	87.1	456	6	ABU47476	ABU47476 Protein e
83	27	87.1	456	6	ABU46912	ABU46912 Protein e
84	27	87.1	457	6	ABU32173	ABU32173 Protein e
85	27	87.1	457	6	ABU15160	ABU15160 Protein e
86	27	87.1	457	8	ADN18076	ADN18076 Bacterial
87	27	87.1	460	2	AAV35220	AAV35220 Chlamydia
88	27	87.1	460	7	ABO66988	ABO66988 Klebsiell
89	27	87.1	463	4	AAU38325	AAU38325 Salmoneil
90	27	87.1	463	6	ABU50389	ABU50389 Protein e
91	27	87.1	463	8	ADN17661	ADN17661 Bacterial
92	27	87.1	463	8	ABO61707	ABO61707 Klebsiell
93	27	87.1	468	8	ADSA27797	ADSA27797 Bacterial
94	27	87.1	483	8	ADSA25210	ADSA25210 Bacterial
95	27	87.1	484	7	ADD22903	ADD22903 T. reesei
96	27	87.1	484	7	ADD22903	ADD22903 T. reesei

97	27	87.1	484	9	AED25788	Aed25788	Trichoder	170	26	83.9	123	4	AU02628	Au02628	Anti-adip
98	27	87.1	488	5	AU79550	Au79550	A. naesli	171	26	83.9	123	9	AED87338	B6 heavy	
99	27	87.1	491	6	ABU41654	Abu41654	Protein e	172	26	83.9	124	9	AD245429	Murine fa	
100	27	87.1	505	8	ADS25873	Ad25873	Bacterial	173	26	83.9	125	2	AAW28065	Staphyloc	
101	27	87.1	505	8	ADS25472	Ad25472	Bacterial	174	26	83.9	125	2	AAJ39818	Llama ant	
102	27	87.1	538	5	ABP39788	Abp39788	Staphyloc	175	26	83.9	125	7	ABO33840	Human ant	
103	27	87.1	538	8	ADSO5529	Adso5529	Staphyloc	176	26	83.9	125	9	AD235786	Anti-glic	
104	27	87.1	545	8	ADX75725	Adx75725	Plant ful	177	26	83.9	126	9	AED63549	Heavy cha	
105	27	87.1	575	8	ADR10067	Adr10067	Human pro	178	26	83.9	127	8	ADO39423	Human AB7	
106	27	87.1	579	4	AAE12776	Aae12776	Chlamydia	179	26	83.9	128	4	AAAG71342	Human sec	
107	27	87.1	592	8	ADJ10121	Adj10121	Rat vitam	180	26	83.9	128	4	AAAG71346	Human sec	
108	27	87.1	607	8	ADS22813	Ad22813	Bacterial	181	26	83.9	128	4	AAAG71348	Human sec	
109	27	87.1	607	8	ADS23171	Ad23171	Bacterial	182	26	83.9	128	4	AAAG71348	Human sec	
110	27	87.1	608	8	ADS23197	Ad23197	Bacterial	183	26	83.9	128	4	AAAG71336	Human sec	
111	27	87.1	608	8	ADS22510	Ad22510	Bacterial	184	26	83.9	128	4	AAAG71334	Human sec	
112	27	87.1	630	4	AAAB76783	Aab76783	Corynebac	185	26	83.9	128	4	AAAG71338	Human sec	
113	27	87.1	630	4	AAAG92305	Ag92305	C. glutami	186	26	83.9	128	4	AAAG71352	Human sec	
114	27	87.1	635	7	ADL65941	Adl65941	C. glutam	187	26	83.9	128	4	AAAG71340	Human sec	
115	27	87.1	635	7	ADL65563	Adl65563	C. glutam	188	26	83.9	128	4	AAAG71344	Human sec	
116	27	87.1	647	6	ABM67463	Abm67463	Phototrab	189	26	83.9	129	9	ADX02195	AAW71045	
117	27	87.1	650	7	ADBE80737	Ad80737	Microsate	190	26	83.9	130	2	AAW71045	Peptide s	
118	27	87.1	650	8	ADJ10123	Adj10123	Pig vitam	191	26	83.9	130	10	AEGB1402	AEGB1402	
119	27	87.1	650	8	ADJ10117	Adj10117	Human vit	192	26	83.9	131	10	AEGB1403	AEGB1403	
120	27	87.1	661	9	AEC59577	Aec59577	Varicella	193	26	83.9	137	6	ABU97068	Recombina	
121	27	87.1	672	5	AAU75887	Aau75887	Human adh	194	26	83.9	140	6	ABG74241	Mouse ant	
122	27	87.1	675	5	ABO80415	Ab080415	Pseudomon	195	26	83.9	142	10	AEGB01479	AEGB01479	
123	27	87.1	912	7	AAW86634	Aw86634	Rice abio	196	26	83.9	142	10	AEGB01504	AEGB01504	
124	27	87.1	1243	6	ABG99964	Abg99964	Human nov	197	26	83.9	143	4	AAAG71354	Human sec	
125	27	87.1	1377	6	ABP56518	Abp56518	Human BAA	198	26	83.9	145	6	ABP78858	Human sec	
126	27	87.1	1421	6	ABO52987	Ab052987	Human put	199	26	83.9	146	5	ABP05286	Human ORF	
127	27	87.1	1556	6	ABO53101	Ab053101	Human put	200	26	83.9	169	4	AAAG76005	Human col	
128	27	87.1	1556	9	ADY25712	ADY25712	MPREN AQR	201	26	83.9	174	8	ADN19577	Bacterial	
129	27	87.1	2190	7	ADB80326	Ad80326	Human MDR	202	26	83.9	189	6	ABP78997	Human sec	
130	26	83.9	10	5	AAU82535	Aau82535	Llama CDR	203	26	83.9	198	4	ABG02424	Novel hum	
131	26	83.9	10	5	AAU82532	Aau82532	Llama CDR	204	26	83.9	198	6	ABP99711	Human sec	
132	26	83.9	28	1	AAU80205	Aau80205	Sequence	205	26	83.9	198	6	ABR01192	Human gen	
133	26	83.9	49	6	ABP77874	Abp77874	N. gonorr	206	26	83.9	198	7	ADC20475	Human sec	
134	26	83.9	50	8	ADH17396	Adh17396	Human NOV	207	26	83.9	199	3	AAAB29815	Human sec	
135	26	83.9	104	4	AAU86940	Aau86940	Human DNA	208	26	83.9	203	2	AAW28268	Amno aci	
136	26	83.9	104	4	AAU87614	Aau87614	Novel cen	209	26	83.9	219	3	AAAG40819	Zea may	
137	26	83.9	104	8	ADT54929	Adt54929	Novel hum	210	26	83.9	229	3	AAAY5611	The nitri	
138	26	83.9	107	3	AAAB41543	Aab41543	Human ORF	211	26	83.9	232	3	AAAB29870	Human sec	
139	26	83.9	108	7	ADFO6021	Adfo6021	Bacterial	212	26	83.9	233	7	AAOB6201	Klebsiell	
140	26	83.9	111	7	ADFO5922	Adfo5922	Bacterial	213	26	83.9	247	1	AAAP80155	Frs and C	
141	26	83.9	117	2	AAU02590	Aau02590	Anti-adip	214	26	83.9	247	1	AAAP80156	Biosynthe	
142	26	83.9	118	2	AAU05237	Aau05237	Testoster	215	26	83.9	247	5	ABP45317	Human Bly	
143	26	83.9	118	2	AAU05238	Aau05238	Testoster	216	26	83.9	247	5	ABP44867	Human Bly	
144	26	83.9	118	2	AAU05235	Aau05235	Testoster	217	26	83.9	247	5	ABP45088	Human Bly	
145	26	83.9	118	2	AAU05236	Aau05236	Testoster	218	26	83.9	247	5	ABP45079	Human Bly	
146	26	83.9	118	4	AAU02530	Aau02530	Anti-adip	219	26	83.9	247	7	ADG95694	Single ch	
147	26	83.9	119	2	AAAR92998	Aar92998	Humanised	220	26	83.9	247	7	ADG95906	Single ch	
148	26	83.9	119	2	AAAR92996	Aar92996	Monoclona	221	26	83.9	247	7	ADG96144	Single ch	
149	26	83.9	119	2	AAW29996	Aaw29996	Humanised	222	26	83.9	247	7	ADG95915	Single ch	
150	26	83.9	119	2	AAW29994	Aaw29994	Heavy cha	223	26	83.9	247	8	ADDO4878	Anti-mous	
151	26	83.9	119	9	AEC76981	Aec76981	Protein e	224	26	83.9	247	8	ADP09937	Anti-mous	
152	26	83.9	119	9	AEC76980	Aec76980	Protein e	225	26	83.9	247	9	AED77747	Human B L	
153	26	83.9	119	10	AEGB08773	Aeg08773	Tie recep	226	26	83.9	247	9	AED77968	Human B L	
154	26	83.9	120	8	ADP09916	Adp09916	Anti-huma	227	26	83.9	247	9	AED77959	Human B L	
155	26	83.9	120	8	ADP09917	Adp09917	Anti-huma	228	26	83.9	247	9	AED78197	Human B L	
156	26	83.9	120	8	ADDO25752	Ado25752	Anti-IFN	229	26	83.9	249	4	AAU35287	Enterococ	
157	26	83.9	120	8	ADDO25751	Ado25751	Anti-IFN	230	26	83.9	249	4	AED30836	Llama ant	
158	26	83.9	120	8	ADDO25875	Ado25875	Camelidae	231	26	83.9	251	3	AAAB43605	Human can	
159	26	83.9	120	8	ADDO25876	Ado25876	Camelidae	232	26	83.9	252	7	ABMB85609	Human pro	
160	26	83.9	120	10	AEGB08921	Aeg08921	Tie recep	233	26	83.9	252	9	ADZ70532	Human pro	
161	26	83.9	121	4	AAU02598	Aau02598	Anti-adip	234	26	83.9	255	5	ABP45188	Human Bly	
162	26	83.9	121	5	ABP30699	Abp30699	Streptoco	235	26	83.9	253	7	ADG96015	Single ch	
163	26	83.9	121	5	ABG61524	Abg61524	Iron upla	236	26	83.9	253	3	AED78068	Human B L	
164	26	83.9	121	6	ABU01471	Abu01471	S. pneumo	237	26	83.9	255	5	ABP45001	Human Bly	
165	26	83.9	121	8	ADY88642	Ady88642	Streptoco	238	26	83.9	255	7	ADG95828	Single ch	
166	26	83.9	121	8	ADY82041	Ady82041	Streptoco	239	26	83.9	255	9	AED77881	Human B L	
167	26	83.9	121	8	ADY79895	Ady79895	Streptoco	240	26	83.9	256	2	ADX02030	SARS coro	
168	26	83.9	122	4	AAAG71350	Aag71350	Human sec	241	26	83.9	264	9	AAU34848	Chlamydia	
169	26	83.9	122	9	AED30809	Aed30809	Llama ant	242	26	83.9	264	6	ABU97152	Recombina	

243	26	83.9	267	6	ABU29331	Abu29331 Protein e	316	26	83.9	473	4	AAG64471	Aag64471 Human cyp
244	26	83.9	271	3	AAG34202	Aag34202 Zee may	317	26	83.9	473	4	AAG64469	Aag64469 Human cyp
245	26	83.9	271	3	AAG40818	Aag40818 DNA mays	318	26	83.9	473	4	AAG64473	Aag64473 Human cyp
246	26	83.9	271	7	ABM74308	Abm74308 Novel sin	319	26	83.9	475	7	ABO63637	Aboc63637 Klebsiell
247	26	83.9	272	9	ADZ58597	Adz58597 Pseudom	320	26	83.9	476	9	ABED19758	Abed19758 Chimeric
248	26	83.9	276	7	ABO76413	Aboc76413 Pseudom	321	26	83.9	495	4	ABG09718	Abg09718 Novel hum
249	26	83.9	279	8	ADX88115	Adx88115 Plant ful	322	26	83.9	495	4	AAH89668	Aah89668 DRCl prot
250	26	83.9	283	7	ABO71739	Aboc71739 Pseudom	323	26	83.9	497	4	AAU37751	Aau37751 Streptoco
251	26	83.9	285	7	ABM65608	Abm65608 Mouse pro	324	26	83.9	497	6	ABU01284	Abu01284 S. pneumo
252	26	83.9	285	7	ABM65608	Abm65608 Mouse pro	325	26	83.9	497	6	ABU45988	Abu45988 Protein e
253	26	83.9	299	8	ADV21133	Adv21133 Human pro	326	26	83.9	497	8	ADK48573	Adk48573 Streptoco
254	26	83.9	303	8	ADP98971	Adp98971 C. albica	327	26	83.9	497	8	ADM92139	Adm92139 S. pneumo
255	26	83.9	307	8	ADO07053	Ado07053 Human pro	328	26	83.9	504	8	ADR95097	Adr95097 Novel S.
256	26	83.9	311	3	AAG34200	Aag34200 Zee mays	329	26	83.9	504	9	AEA58967	Aea58967 Streptoco
257	26	83.9	315	8	ADN36928	Adn36928 X. albii	330	26	83.9	506	7	ABO61660	Aboc61660 Klebsiell
258	26	83.9	319	8	ABM65481	Abm65481 Fusion ge	331	26	83.9	509	6	ABJ18916	Abj18916 Pathogen
259	26	83.9	319	4	AAAB67541	Aaab67541 Amino aci	332	26	83.9	509	6	ABM72709	Abm72709 Staphyloc
260	26	83.9	321	7	ADB70077	Adb70077 C. neofor	333	26	83.9	509	6	ABM72584	Abm72584 Staphyloc
261	26	83.9	327	7	ABO67488	Aboc67488 Klebsiell	334	26	83.9	520	6	ABM73438	Abm73438 Staphyloc
262	26	83.9	328	3	ABM36480	Abm36480 Fusion ge	335	26	83.9	528	6	ABJ26447	Abj26447 Aspergill
263	26	83.9	328	4	AAAB67540	Aaab67540 Amino aci	336	26	83.9	543	6	ABU31756	Abu31756 Protein e
264	26	83.9	335	4	AAU87326	Aau87326 Novel cen	337	26	83.9	544	7	ABO80249	Aboc80249 Pseudom
265	26	83.9	335	8	AD154641	Ad154641 Novel hum	338	26	83.9	547	5	AAE14507	Aae14507 Human car
266	26	83.9	336	5	ABG63444	Abg63444 Human gen	339	26	83.9	547	7	ABO64232	Aboc64232 Klebsiell
267	26	83.9	336	5	ADL76709	Adl76709 Albumin f	340	26	83.9	547	8	AD179888	Ad179888 Protein o
268	26	83.9	339	5	ABG72018	Abg72018 Mouse cha	341	26	83.9	549	7	ABH80159	Abh80159 Mycobacte
269	26	83.9	340	5	ABP39211	Abp39211 Staphyloc	342	26	83.9	557	4	ABG07424	Abg07424 Novel hum
270	26	83.9	340	8	ADS05826	Ads05826 Staphyloc	343	26	83.9	557	7	ADG42192	Adg42192 Human bta
271	26	83.9	341	6	ADA36377	Ada36377 Acinetoba	344	26	83.9	558	8	ADN20745	Adn20745 Bacteri
272	26	83.9	342	8	ADO28579	Ado28579 Human pro	345	26	83.9	571	3	AAV71107	Aav71107 Human Hyd
273	26	83.9	342	8	ADX65968	Adx65968 Plant ful	346	26	83.9	571	3	AAAB18914	Aaab18914 A novel p
274	26	83.9	342	9	AECL1995	Aecl1995 Rat surro	347	26	83.9	571	4	AAU12442	Aau12442 Human PRO
275	26	83.9	342	9	AECL1571	Aecl1571 Rat surro	348	26	83.9	571	4	AAE04101	Aae04101 Human gen
276	26	83.9	342	10	AECL1996	Aecl1996 Rat surro	349	26	83.9	571	5	AAUB3696	Aau3696 Human PRO
277	26	83.9	342	10	AEF27704	Aef27704 Rat prost	350	26	83.9	571	5	ABH84949	Abh84949 Human PRO
278	26	83.9	342	10	ABG96402	Abg96402 Human ova	351	26	83.9	571	5	ABG64341	Abg64341 Human alb
279	26	83.9	343	5	ABU78547	Abu78547 Human pro	352	26	83.9	571	5	ADY31950	Ady31950 Novel hum
280	26	83.9	343	5	ABU78547	Abu78547 Human pro	353	26	83.9	571	6	ABO17866	Aboc17866 Novel hum
281	26	83.9	343	5	ABBO7285	Abbo7285 Amino aci	354	26	83.9	571	6	ABU69108	Abu69108 Human PRO
282	26	83.9	343	6	ABJ37067	Abj37067 Human bre	355	26	83.9	571	6	ABU80843	Abu80843 Human PRO
283	26	83.9	343	7	ADD47565	Add47565 Human pro	356	26	83.9	571	6	ABO33809	Aboc33809 Novel hum
284	26	83.9	343	7	ADD47561	Add47561 Human pro	357	26	83.9	571	6	ABU81140	Abu81140 Human PRO
285	26	83.9	343	7	ADG38955	Adg38955 Human pro	358	26	83.9	571	6	ABO19424	Aboc19424 Human sec
286	26	83.9	343	8	ADN03871	Adn03871 Antipsoxi	359	26	83.9	571	6	ABU66840	Abu66840 Human PRO
287	26	83.9	343	8	ADV25080	Adv25080 Human ser	360	26	83.9	571	6	ABU59921	Abu59921 Novel sec
288	26	83.9	343	9	AECL1215	Aecl1215 Human sur	361	26	83.9	571	6	ABO69085	Aboc69085 Human PRO
289	26	83.9	343	9	AECL1215	Aecl1215 Human sur	362	26	83.9	571	6	ABO25111	Aboc25111 Human sec
290	26	83.9	343	9	AECL1217	Aecl1217 Human sur	363	26	83.9	571	6	ABU62152	Abu62152 Novel hum
291	26	83.9	343	10	AEF72276	Aef72276 Human tar	364	26	83.9	571	6	ABU67116	Abu67116 Human sec
292	26	83.9	343	10	AEF27700	Aef27700 Human pro	365	26	83.9	571	6	ABU81549	Abu81549 Human sec
293	26	83.9	348	6	ABU18926	Abu18926 Pathogen	366	26	83.9	571	6	ADA46061	Ada46061 Novel hum
294	26	83.9	348	6	ABM72980	Abm72980 Staphyloc	367	26	83.9	571	6	ADA76548	Ada76548 Novel hum
295	26	83.9	349	8	ADT59250	Adt59250 Plant pol	368	26	83.9	571	6	ADA76492	Ada76492 Human PRO
296	26	83.9	356	8	ADN20668	Adn20668 Bacteri	369	26	83.9	571	6	ABJ72332	Abj72332 Human PRO
297	26	83.9	363	7	ABO84037	Aboc84037 Pseudom	370	26	83.9	571	6	ADA19142	Ada19142 Human PRO
298	26	83.9	365	8	ADO57564	Ado57564 Actinobac	371	26	83.9	571	6	ADA61765	Ada61765 Homo sapi
299	26	83.9	376	8	ABM91934	Abm91934 M. xanthu	372	26	83.9	571	6	ADB19550	Adb19550 Novel hum
300	26	83.9	386	5	ABE98416	Abbe98416 Human NOV	373	26	83.9	571	6	ADB28091	Adb28091 Human PRO
301	26	83.9	393	7	ADF06202	Adf06202 Bacteri	374	26	83.9	571	6	ADA68570	Ada68570 Novel hum
302	26	83.9	393	7	AED74215	Aed74215 Human pla	375	26	83.9	571	6	ADBI6134	Adbi6134 Human PRO
303	26	83.9	431	5	ABBA8085	Abba8085 Listeria	376	26	83.9	571	6	ADA47920	Ada47920 Human PRO
304	26	83.9	435	7	AAAB20163	Aaab20163 Human pro	377	26	83.9	571	6	ADA67715	Ada67715 Human PRO
305	26	83.9	445	7	ADG38848	Adg38848 Human SEC	378	26	83.9	571	6	ADB30722	Adb30722 Human PRO
306	26	83.9	448	6	ABU44929	Abu44929 Protein e	379	26	83.9	571	6	ADA86018	Ada86018 Novel hum
307	26	83.9	450	8	ADS30536	Ads30536 Bacteri	380	26	83.9	571	6	ADA97230	Ada97230 Human PRO
308	26	83.9	451	8	ADH17410	Adh17410 Human NOV	381	26	83.9	571	6	ADA79534	Ada79534 Human PRO
309	26	83.9	451	8	ADH17412	Adh17412 Human NOV	382	26	83.9	571	6	ADA87673	Ada87673 Novel hum
310	26	83.9	451	8	ADH17394	Adh17394 Human NOV	383	26	83.9	571	6	ADA16875	Ada16875 Human PRO
311	26	83.9	463	8	ADM72025	Adm72025 Chimeric	384	26	83.9	571	6	ADA91967	Ada91967 Novel hum
312	26	83.9	463	10	AEF50991	Aef50991 Variable	385	26	83.9	571	6	ADBI5030	Adbi5030 Human PRO
313	26	83.9	466	1	AAAP40032	Aap40032 Gamma ant	386	26	83.9	571	6	ADBI8991	Adbi8991 Novel hum
314	26	83.9	467	6	ABU41994	Abu41994 Protein e	387	26	83.9	571	6	ADA94206	Ada94206 Human PRO
315	26	83.9	473	4	AAG64475	Aag64475 Human typ	388	26	83.9	571	6	ADB20102	Adb20102 Novel hum

389	26	83.9	571	6	ADB13414	Adh13414	Human	PRO
390	26	83.9	571	6	ABO43419	AbO43419	Novel	hum
391	26	83.9	571	6	ADA74668	AdA74668	Human	PRO
392	26	83.9	571	6	ADB24901	AdB24901	Human	PRO
393	26	83.9	571	6	ADA82425	AdA82425	Human	PRO
394	26	83.9	571	6	ADA75388	AdA75388	Human	PRO
395	26	83.9	571	6	ADA85466	AdA85466	Novel	hum
396	26	83.9	571	6	ADA84914	AdA84914	Novel	hum
397	26	83.9	571	6	ADB30170	AdB30170	Human	PRO
398	26	83.9	571	6	ADA80698	AdA80698	Human	PRO
399	26	83.9	571	6	ADA75940	AdA75940	Human	PRO
400	26	83.9	571	6	ADA47165	AdA47165	Human	PRO
401	26	83.9	571	6	ADB25461	AdB25461	Human	PRO
402	26	83.9	571	6	ADA93637	AdA93637	Human	PRO
403	26	83.9	571	6	ADB26987	AdB26987	Human	PRO
404	26	83.9	571	6	ADB31274	AdB31274	Human	PRO
405	26	83.9	571	6	ABJ72460	AbJ72460	Human	PRO
406	26	83.9	571	6	ADA61202	AdA61202	Homo sapi	
407	26	83.9	571	6	ADB24349	AdB24349	Human	PRO
408	26	83.9	571	6	ADA96678	AdA96678	Human	PRO
409	26	83.9	571	6	ADA81250	AdA81250	Human	PRO
410	26	83.9	571	6	ADA96126	AdA96126	Human	PRO
411	26	83.9	571	6	ADB26435	AdB26435	Human	PRO
412	26	83.9	571	6	ADB21920	AdB21920	Novel	hum
413	26	83.9	571	6	ABO34355	AbO34355	Human	sec
414	26	83.9	571	7	ADA77699	AdA77699	Human	PRO
415	26	83.9	571	7	ADB18439	AdB18439	Human	PRO
416	26	83.9	571	7	ADA87122	AdA87122	Novel	hum
417	26	83.9	571	7	ABO25132	AbO25132	Human	sec
418	26	83.9	571	7	ADA88825	AdA88825	Novel	hum
419	26	83.9	571	7	ADA46613	AdA46613	Novel	hum
420	26	83.9	571	7	ADB28643	AdB28643	Human	PRO
421	26	83.9	571	7	ADB29195	AdB29195	Human	PRO
422	26	83.9	571	7	ADA77147	AdA77147	Human	PRO
423	26	83.9	571	7	ADA88777	AdA88777	Novel	hum
424	26	83.9	571	7	ADA97782	AdA97782	Human	PRO
425	26	83.9	571	7	ADB27539	AdB27539	Human	PRO
426	26	83.9	571	7	ADB22472	AdB22472	Novel	hum
427	26	83.9	571	7	ABJ72162	AbJ72162	Human	mem
428	26	83.9	571	7	ADA67163	AdA67163	Human	PRO
429	26	83.9	571	7	ADB23024	AdB23024	Human	PRO
430	26	83.9	571	7	ADB23797	AdB23797	Human	PRO
431	26	83.9	571	7	ADA92519	AdA92519	Novel	hum
432	26	83.9	571	7	ADB15582	AdB15582	Human	PRO
433	26	83.9	571	7	ADB83700	AdB83700	Novel	hum
434	26	83.9	571	7	ADB80806	AdB80806	Novel	hum
435	26	83.9	571	7	ADB73347	AdB73347	Novel	hum
436	26	83.9	571	7	ADB38834	AdB38834	Novel	hum
437	26	83.9	571	7	ADB78429	AdB78429	Novel	hum
438	26	83.9	571	7	ADB38282	AdB38282	Novel	hum
439	26	83.9	571	7	ADB66754	AdB66754	Novel	hum
440	26	83.9	571	7	ADB85077	AdB85077	Human	PRO
441	26	83.9	571	7	ADB89834	AdB89834	Human	PRO
442	26	83.9	571	7	ADB90566	AdB90566	Human	PRO
443	26	83.9	571	7	ADB39667	AdB39667	Novel	hum
444	26	83.9	571	7	ADB78183	AdB78183	Novel	hum
445	26	83.9	571	7	ADB87249	AdB87249	Human	PRO
446	26	83.9	571	7	ADB84831	AdB84831	Human	PRO
447	26	83.9	571	7	ADB47290	AdB47290	Novel	hum
448	26	83.9	571	7	ADB83946	AdB83946	Novel	hum
449	26	83.9	571	7	ADB86897	AdB86897	Human	PRO
450	26	83.9	571	7	ADB73101	AdB73101	Novel	hum
451	26	83.9	571	7	ADB77502	AdB77502	Novel	hum
452	26	83.9	571	7	ADB34659	AdB34659	Human	PRO
453	26	83.9	571	7	ADB35763	AdB35763	Human	PRO
454	26	83.9	571	7	ADB34107	AdB34107	Human	PRO
455	26	83.9	571	7	ADB35211	AdB35211	Human	PRO
456	26	83.9	571	7	ADB36315	AdB36315	Human	PRO
457	26	83.9	571	7	ADB46710	AdB46710	Novel	hum
458	26	83.9	571	7	AAE39102	Aae39102	Human	PRO
459	26	83.9	571	7	AAE39039	Aae39039	Human	PRO
460	26	83.9	571	7	ADC36939	AdC36939	Human	PRO
461	26	83.9	571	7	ADC21929	AdC21929	Human	PRO

462	26	83.9	571	7	ADC50583	AdC50583	Novel	hum
463	26	83.9	571	7	ADC72130	AdC72130	Novel	hum
464	26	83.9	571	7	ADC29779	AdC29779	Novel	hum
465	26	83.9	571	7	ADC60109	AdC60109	Novel	hum
466	26	83.9	571	7	ADC49960	AdC49960	Novel	hum
467	26	83.9	571	7	ADC49159	AdC49159	Novel	hum
468	26	83.9	571	7	ADC49676	AdC49676	Novel	hum
469	26	83.9	571	7	ADC47537	AdC47537	Novel	hum
470	26	83.9	571	7	ADC51116	AdC51116	Novel	hum
471	26	83.9	571	7	ADC57470	AdC57470	Novel	hum
472	26	83.9	571	7	ADC60661	AdC60661	Novel	hum
473	26	83.9	571	7	ADC51136	AdC51136	Novel	hum
474	26	83.9	571	7	ADC65663	AdC65663	Human	PRO
475	26	83.9	571	7	ADC54761	AdC54761	Novel	hum
476	26	83.9	571	7	ADC53722	AdC53722	Novel	hum
477	26	83.9	571	7	ADC59245	AdC59245	Novel	hum
478	26	83.9	571	7	ADC56123	AdC56123	Novel	hum
479	26	83.9	571	7	ADC58693	AdC58693	Novel	hum
480	26	83.9	571	7	ADC47282	AdC47282	Novel	hum
481	26	83.9	571	7	ADC03367	AdC03367	Novel	hum
482	26	83.9	571	7	ADC90359	AdC90359	Novel	hum
483	26	83.9	571	7	ADC69778	AdC69778	Human	PRO
484	26	83.9	571	7	ADC48667	AdC48667	Human	PRO
485	26	83.9	571	7	ADD10196	AdD10196	Human	PRO
486	26	83.9	571	7	ADC78157	AdC78157	Novel	hum
487	26	83.9	571	7	ADD04771	AdD04771	Novel	hum
488	26	83.9	571	7	ADD06392	AdD06392	Novel	hum
489	26	83.9	571	7	ADC80727	AdC80727	Novel	hum
490	26	83.9	571	7	ADD11234	AdD11234	Human	PRO
491	26	83.9	571	7	ADD10555	AdD10555	Human	sec
492	26	83.9	571	7	ADC48115	AdC48115	Human	PRO
493	26	83.9	571	7	ADC77911	AdC77911	Novel	hum
494	26	83.9	571	7	ADC80175	AdC80175	Novel	hum
495	26	83.9	571	7	ADD11515	AdD11515	Human	sec
496	26	83.9	571	7	ADD09644	AdD09644	Human	PRO
497	26	83.9	571	7	ADD50874	AdD50874	Novel	hum
498	26	83.9	571	7	ADD41357	AdD41357	Novel	hum
499	26	83.9	571	7	ADD52496	AdD52496	Human	PRO
500	26	83.9	571	7	ADD51120	AdD51120	Novel	hum

ALIGNMENTS

RESULT 1								
ID	ADQ90196	standard; peptide; 6 AA.						
AC	ADQ90196;							
XX								
DT	21-OCT-2004	(first entry)						
XX								
DE	FSRYAR 6 mer domain motoneuronotrophic factor peptide analogue.							
XX								
KW	motoneuronotrophic; motor neuron; Neurotrophic; Neuroprotective; Vulnerary;							
KW	Neuropeptide-Agonist; axon degeneration; muscle reinnervation;							
XX	peripheral nerve; neurodegenerative; wound healing.							
OS	Unidentified.							
XX								
PN	WO2004065410-A2.							
XX								
PD	05-AUG-2004.							
XX								
PF	21-JAN-2004; 2004WO-US001468.							
XX								
PR	21-JAN-2003; 2003US-0441772P.							
PA	(GENE-) GENERVON BIOPHARMACEUTICALS LLC.							
XX								
PI	Chau RMW, Ko TD;							
XX								
DR	WPI; 2004-562147/54.							

XX New motoneuronotrophic factor peptide analogue enhancing the viability of
PT motor neurons, useful for target muscle reinnervation, treating
PT peripheral nerve injuries or neurodegenerative diseases and in wound
PT healing.
XX
PS Claim 1; SEQ ID NO 2; 40pp; English.
XX
CC The present invention relates to motoneuronotrophic factor peptide
CC analogue, where the peptide analogue enhances the viability of motor
CC neurons. The methods and compositions of the present invention are useful
CC for promoting motor neuron viability and axon degeneration, target muscle
CC reinnervation, treating peripheral nerve injuries, treating
CC neurodegenerative disease and in wound healing. The present sequence
CC represents FSRYPAR 6 mer domain motoneuronotrophic factor peptide
CC analogue.
XX
SQ Sequence 6 AA:
XX
Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FSRYPAR 6
DB 1 FSRYPAR 6
XX
RESULT 2
ADQ90198
ID ADQ90198 standard; peptide; 10 AA.
XX
AC ADQ90198;
XX
DT 21-OCT-2004 (first entry)
XX
DE MNTF 10 mer motoneuronotrophic factor peptide analogue.
XX
KM motoneuronotrophic; motor neuron; Neurotrophic; Neuroprotective; Vulnerary;
KM Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
KW peripheral nerve; neurodegenerative; wound healing.
XX
OS Unidentified.
XX
PN WO2004065410-A2.
XX
PD 05-AUG-2004.
XX
PF 21-JAN-2004; 2004WO-US001468.
XX
PR 21-JAN-2003; 2003US-0441772P.
XX
PA (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
XX
PI Chau RMW, Ko TD;
XX
DR WPI; 2004-562147/54.
XX
PT New motoneuronotrophic factor peptide analogue enhancing the viability of
PT motor neurons, useful for target muscle reinnervation, treating
PT peripheral nerve injuries or neurodegenerative diseases and in wound
PT healing.
XX
PS Claim 7; SEQ ID NO 4; 40pp; English.
XX
CC The present invention relates to motoneuronotrophic factor peptide
CC analogue, where the peptide analogue enhances the viability of motor
CC neurons. The methods and compositions of the present invention are useful
CC for promoting motor neuron viability and axon degeneration, target muscle
CC reinnervation, treating peripheral nerve injuries, treating
CC neurodegenerative disease and in wound healing. The present sequence
CC represents a MNTF motoneuronotrophic factor peptide analogue.
XX

SQ Sequence 10 AA;
XX
Query Match 100.0%; Score 31; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FSRYPAR 6
DB 5 FSRYPAR 10
XX
RESULT 3
ADQ90199
ID ADQ90199 standard; peptide; 11 AA.
XX
AC ADQ90199;
XX
DT 21-OCT-2004 (first entry)
XX
DE MNTF 11 mer motoneuronotrophic factor peptide analogue.
XX
KM motoneuronotrophic; motor neuron; Neurotrophic; Neuroprotective; Vulnerary;
KM Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
KW peripheral nerve; neurodegenerative; wound healing.
XX
OS Unidentified.
XX
PN WO2004065410-A2.
XX
PD 05-AUG-2004.
XX
PF 21-JAN-2004; 2004WO-US001468.
XX
PR 21-JAN-2003; 2003US-0441772P.
XX
PA (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
XX
PI Chau RMW, Ko TD;
XX
DR WPI; 2004-562147/54.
XX
PT New motoneuronotrophic factor peptide analogue enhancing the viability of
PT motor neurons, useful for target muscle reinnervation, treating
PT peripheral nerve injuries or neurodegenerative diseases and in wound
PT healing.
XX
PS Claim 7; SEQ ID NO 5; 40pp; English.
XX
CC The present invention relates to motoneuronotrophic factor peptide
CC analogue, where the peptide analogue enhances the viability of motor
CC neurons. The methods and compositions of the present invention are useful
CC for promoting motor neuron viability and axon degeneration, target muscle
CC reinnervation, treating peripheral nerve injuries, treating
CC neurodegenerative disease and in wound healing. The present sequence
CC represents a MNTF motoneuronotrophic factor peptide analogue.
XX
SQ Sequence 11 AA;
XX
Query Match 100.0%; Score 31; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FSRYPAR 6
DB 1 FSRYPAR 6
XX
RESULT 4
ADQ90200
ID ADQ90200 standard; peptide; 13 AA.
XX
AC ADQ90200;
XX

DT 21-OCT-2004 (first entry)
 XX MNTF 13 mer motoneuronotrophic factor peptide analogue.
 DE
 XX
 XX motoneuronotrophic; motor neuron; Neurotrophic; Neuroprotective; Vulnerary;
 KM Neuropptide-Agonist; axon degeneration; muscle reinnervation;
 KM peripheral nerve; neurodegenerative; wound healing.
 OS Unidentified.
 XX WO2004065410-A2.
 PN 05-AUG-2004.
 PD 21-JAN-2004; 2004WO-US001468.
 PF 21-JAN-2003; 2003US-0441772P.
 PR (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
 PA Chau RMW, Ko TD;
 PI WPI; 2004-562147/54.
 DR
 XX New motoneuronotrophic factor peptide analogue enhancing the viability of
 PT motor neurons, useful for target muscle reinnervation, treating
 PT peripheral nerve injuries or neurodegenerative diseases and in wound
 PT healing.
 PS Claim 7; SEQ ID NO 6; 40bp; English.
 XX
 XX The present invention relates to motoneuronotrophic factor peptide
 CC analogue, where the peptide analogue enhances the viability of motor
 CC neurons. The methods and compositions of the present invention are useful
 CC for promoting motor neuron viability and axon degeneration, target muscle
 CC reinnervation, treating peripheral nerve injuries, treating
 CC neurodegenerative disease and in wound healing. The present sequence
 CC represents a MNTF motoneuronotrophic factor peptide analogue.
 CC
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 31; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 Db 7 FSRYAR 12
 RESULT 5
 ADQ90201
 ID ADQ90201 standard; peptide; 21 AA.
 AC ADQ90201;
 XX 21-OCT-2004 (first entry)
 DT MNTF 21 mer motoneuronotrophic factor peptide analogue.
 DE
 XX motoneuronotrophic; motor neuron; Neurotrophic; Neuroprotective; Vulnerary;
 KM Neuropptide-Agonist; axon degeneration; muscle reinnervation;
 KM peripheral nerve; neurodegenerative; wound healing.
 XX Unidentified.
 OS
 XX WO2004065410-A2.
 PN 05-AUG-2004.
 PD 21-JAN-2004; 2004WO-US001468.
 PF 21-JAN-2003; 2003US-0441772P.
 PR 21-JAN-2003; 2003US-0441772P.

XX (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
 PA Chau RMW, Ko TD;
 PI WPI; 2004-562147/54.
 DR
 XX New motoneuronotrophic factor peptide analogue enhancing the viability of
 PT motor neurons, useful for target muscle reinnervation, treating
 PT peripheral nerve injuries or neurodegenerative diseases and in wound
 PT healing.
 PS Claim 7; SEQ ID NO 7; 40bp; English.
 XX
 XX The present invention relates to motoneuronotrophic factor peptide
 CC analogue, where the peptide analogue enhances the viability of motor
 CC neurons. The methods and compositions of the present invention are useful
 CC for promoting motor neuron viability and axon degeneration, target muscle
 CC reinnervation, treating peripheral nerve injuries, treating
 CC neurodegenerative disease and in wound healing. The present sequence
 CC represents a MNTF motoneuronotrophic factor peptide analogue.
 CC
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 31; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 Db 5 FSRYAR 10
 RESULT 6
 AEA17675
 ID AEA17675 standard; protein; 21 AA.
 AC AEA17675;
 XX 28-JUL-2005 (first entry)
 DT Motoneuronotrophic factor (MNTF) polypeptide, SEQ ID NO:29.
 DE
 XX motoneuronotrophic factor; MNTF; cell growth; cell proliferation;
 KM DNA detection; chromosome 16.
 XX Homo sapiens.
 OS
 XX WO2005047487-A2.
 PN 26-MAY-2005.
 PD 08-NOV-2004; 2004WO-US038651.
 PF 07-NOV-2003; 2003US-0518581P.
 PR (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
 PA Xue BB;
 PI WPI; 2005-386358/39.
 DR New isolated polynucleotide consisting of a motoneuronotrophic factor
 XX (MNTF)-associated nucleic acid sequence, useful for promoting the
 PT survival, growth, proliferation and maintenance of mammalian neurons.
 PT
 XX Claim 7; SEQ ID NO 29; 34bp; English.
 PS
 XX The invention relates to an isolated polynucleotide consisting of a
 CC motoneuronotrophic factor (MNTF)-associated nucleic acid sequence
 CC comprising AEA17647 or AEA17648, its fragment or complement. Also
 CC described are the following: a composition comprising a first and second
 CC polynucleotide, the first polynucleotide containing an open reading frame

CC : an isolated MNTF associated polypeptide encoded by an open reading
 CC frame of SEQ ID No. 1, a fusion protein comprising an MNTF associated
 CC polypeptide encoded by an open reading frame of SEQ ID no. 1 linked to a
 CC heterologous protein; an expression vector operably linked to the
 CC isolated polynucleotide, where at least one open reading frame is
 CC operably linked to a control sequence compatible with a desired host
 CC vector; an isolated host cell transformed with the expression vector; a
 CC method for determining the presence of a MNTF-associated polynucleotide
 CC in a medium; a method of comparing the relative abundance of MNTF
 CC associated expression products in different samples; and a panel for use
 CC in hybridization assay comprising two or more polynucleotides stably
 CC associated with the surface of a solid support. The polynucleotides are
 CC useful for promoting the survival, growth, proliferation and maintenance
 CC of mammalian neurons. The present sequence represents a polypeptide
 CC encoded by an open reading frame of MNTF cDNA (see ABA1/647), which is
 CC located on chromosome 16q22.

XX Sequence 21 AA;

Query Match 100.0%; Score 31; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
 |||||
 Db 5 FSRYAR 10

RESULT 7

AAWS9046 ID AAW59046 standard; protein; 33 AA.

XX AAW59046;

DT 11-AUG-1998 (first entry)

XX Human MNTF1-F6 protein fragment.

XX Motoneuronotrophic factor; MNTF-1; MNTF1-F6; human; axon regeneration;
 KM motoneuron; diagnose; treatment; disease; wound healing; scar tissue;
 KM keloid.

XX Homo sapiens.

XX WO9813492-A2.

XX 02-APR-1998.

PD 22-SEP-1997; 97WO-US017142.

PF 27-SEP-1996; 96US-0026792P.

PR 15-NOV-1996; 96US-00751225.

PR 12-SEP-1997; 97US-00928862.

XX (KMBI-) KM BIOTECH INC.

PA Chau RMW;

XX MPI; 1998-230703/20.

DR N-PSDB; AAV11748.

XX Motoneuronotrophic factor MNTF1-F3 and MNTF1-F6 - useful for motoneuron
 PT regeneration, diagnosing or treating motoneuron disease and to accelerate
 PT wound healing without scar formation.

XX Claim 4; Fig 2B; 78pp; English.

XX This sequence, represents a fragment of a novel human motoneuronotrophic
 CC factor, MNTF1-F6. Such factors are used to promote regeneration of the
 CC axon of a motoneuron, to diagnose and treat motoneuron disease in a
 CC mammal or to accelerate wound healing whilst concomitantly minimising or
 CC inhibiting scar tissue and/or keloid formation in an area associated with
 CC a wound. For promoting axonal regeneration, the polypeptide is

CC administered at a concentration of 5 ng-50 mg, whereas for inhibiting
 CC hereditary motoneuron disease, the dosage is 5-100 (especially 30-50)ng
 CC per kg body weight

XX Sequence 33 AA;

Query Match 100.0%; Score 31; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
 |||||
 Db 17 FSRYAR 22

RESULT 8

AAO29914 ID AAO29914 standard; protein; 33 AA.

XX AAO29914;

DT 03-SEP-2003 (first entry)

XX Human motoneuronotrophic factor (MNTF)1-F6 protein.

XX Human; motoneuronotrophic factor; MNTF; therapy; radiation therapy;
 KM peripheral nerve injury; musculoskeletal disorder; spinal cord injury;
 KM head injury; stroke; neuromuscular degenerative disease; noctropic;
 KM amyotrophic lateral sclerosis; peripheral neuropathy; neuroprotective;
 KM muscular dystrophy; AIDS; spinal muscular atrophy; multiple sclerosis;
 KM scar; myasthenia gravis; sensory neuronal function disorder; vulnary;
 KM cancer.

XX Homo sapiens.

XX WO2003044175-A2.

XX 30-MAY-2003.

PD 19-NOV-2002; 2002WO-US037191.

PF 20-NOV-2001; 2001US-00989481.

PR (GENE-) GENERON BIOPHARMACEUTICALS LLC.

PA Chau RMW;

XX MPI; 2003-457607/43.

XX N-PSDB; AAL60573.

XX Claim 1; Fig 2B; 90pp; English.

XX The invention relates to a method for promoting the survival, growth,
 CC proliferation or maintenance of mammalian neurons by administering
 CC motoneuronotrophic factors (MNTF). The method is useful for treating
 CC peripheral nerve injuries, musculoskeletal disorders, spinal cord
 CC injuries, head injuries, strokes, neuromuscular degenerative diseases,
 CC amyotrophic lateral sclerosis, spinal muscular atrophy, peripheral
 CC neuropathy, diabetic peripheral neuropathy, peripheral neuropathy
 CC resulting from AIDS or radiation therapy for cancer, multiple sclerosis,
 CC muscular dystrophy, inhibition of scar formation, myasthenia gravis and
 CC sensory neuronal function disorders. The present sequence is human MNTF1-
 CC F6 protein used to illustrate the method of the invention

XX Sequence 33 AA;

XX Query Match 100.0%; Score 31; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 FSRYAR 6
      |||||
Db      17 FSRYAR 22

RESULT 9
ADQ90195 ADQ90195 standard; peptide; 33 AA.
XX
AC ADQ90195;
XX
DT 21-OCT-2004 (first entry)
XX
DE MNTF1-F6 33 mer motoneuronotrophic factor peptide analogue.
XX
KW motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnerary;
KW Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
KW peripheral nerve; neurodegenerative; wound healing.
XX
OS Unidentified.
XX
PN MO2004065410-A2.
XX
PD 05-AUG-2004.
XX
PF 21-JAN-2004; 2004WO-US001468.
XX
PR 21-JAN-2003; 2003US-0441772P.
XX
PA (GENE-) GENEVRON BIOPHARMACEUTICALS LLC.
XX
PI Chau RMM, Ko TD;
XX
DR WPI; 2004-562147/54.
XX
PT New motoneuronotrophic factor peptide analogue enhancing the viability of
PT motor neurons, useful for target muscle reinnervation, treating
PT peripheral nerve injuries or neurodegenerative diseases and in wound
PT healing.
XX
PS Claim 2; SEQ ID NO 1; 40pp; English.
XX
CC The present invention relates to motoneuronotrophic factor peptide
CC analogue, where the peptide analogue enhances the viability of motor
CC neurons. The methods and compositions of the present invention are useful
CC for promoting motor neuron viability and axon degeneration, target muscle
CC reinnervation, treating peripheral nerve injuries, treating muscle
CC neurodegenerative disease and in wound healing. The present sequence
CC represents MNTF1-F6 33 mer motoneuronotrophic factor peptide analogue.
XX
SQ Sequence 33 AA;

Query Match      100.0%; Score 31; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRYAR 6
      |||||
Db      17 FSRYAR 22

RESULT 10
AAU57756 AAU57756 standard; protein; 81 AA.
XX
AC AAU57756;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #18652.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

```

```

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PE 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bharia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59585.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 18951; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences
XX
SQ Sequence 81 AA;

Query Match      100.0%; Score 31; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRYAR 6
      |||||
Db      14 FSRYAR 19

RESULT 11
ABM54275 ABM54275 standard; protein; 81 AA.
XX
AC ABM54275;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #18951.
XX
KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;

```

KM immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL,
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Valiieve-Douglas J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64514.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 18951; 1481bp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 81 AA;
XX
Query Match 100.0%; Score 31; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYAR 6
Db 14 FSRYAR 19
XX
RESULT 12
AAU57258
ID AAU57258 standard; protein; 112 AA.
XX
AC AAU57258;
XX
DT 27-FEB-2002 (first entry)

XX
DE Propionibacterium acnes immunogenic protein #18154.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KM dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L.maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59581.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 112 AA;
XX
Query Match 100.0%; Score 31; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYAR 6
Db 35 FSRYAR 40
XX
RESULT 13
ABM53777
ID ABM53777 standard; protein; 112 AA.
XX
AC ABM53777;
XX
DT 20-OCT-2003 (first entry)

XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #18453.
 XX AC Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX KM immunostimulant; immune response; vaccine.
 XX OS Propionibacterium acnes.
 XX PN WO2003033515-A1.
 XX PD 24-APR-2003.
 XX PF 11-OCT-2002; 2002WO-US032727.
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vaille-Douglas J;
 XX WPI: 2003-381789/36.
 DR N-PSDB: ACF64510.
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX Example 1; SEQ ID NO 18453; 1481bp; English.
 PS The invention relates to an isolated polynucleotide (ACF6435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 112 AA;
 Query Match 100.0%; Score 31; DB 6; Length 112;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 Db 35 FSRYAR 40

RESULT 14
 ABM64633
 ID ABM64633 standard; protein; 174 AA.

XX AC ABM64633;
 XX AC 20-OCT-2003 (first entry)
 XX DE Propionibacterium acnes immunogenic polypeptide #29309.
 XX KM Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX KW immunostimulant; immune response; vaccine; immunogenic.
 XX OS Propionibacterium acnes.
 XX PN WO2003033515-A1.
 XX PD 24-APR-2003.
 XX PF 11-OCT-2002; 2002WO-US032727.
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vaille-Douglas J;
 XX WPI: 2003-381789/36.
 DR New Propionibacterium acnes polypeptides and polynucleotides encoding the
 DR polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 DR or for stimulating an immune response specific for a P. acnes protein.
 XX Claim 7; SEQ ID NO 29309; 1481bp; English.
 PS The invention relates to an isolated polynucleotide (ACF6435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a specifically claimed P. acnes polypeptide which is
 CC thought to contain an immunogenic region. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 174 AA;
 Query Match 100.0%; Score 31; DB 6; Length 174;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 Db 35 FSRYAR 40

```

RESULT 15
AAV35559
ID AAV35559 standard; protein; 357 AA.
XX
XX AAV35559;
AC
XX 17-OCT-2003 (revised)
DT 13-SEP-1999 (first entry)
XX
DE Chlamydia pneumoniae transmembrane protein sequence.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX WO9927105-A2.
XX
XX 03-JUN-1999.
PD
XX
XX 20-NOV-1998; 98WO-IB001890.
PF
XX
XX 21-NOV-1997; 97FR-00014673.
PR
XX 04-NOV-1998; 98US-0107078P.
PR
XX
XX (GEST ) GENSET.
PA
XX
XX Griflais R;
PI
XX
XX WPI; 1999-357842/30.
DR
XX
XX Genome sequence of Chlamydia pneumoniae.
PT
XX
XX Page 1303-1304; Disclosure; 1912pp; English.
PS
XX
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
CC
XX
XX Sequence 357 AA;
SQ
Query Match 100.0%; Score 31; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYAR 6
Db 135 FSRYAR 140

```

```

KM cerebrovascular disease; aortic aneurysm; claudication; stroke;
XX strain CWL029.
XX
XX Chlamydia pneumoniae.
OS
XX WO200202606-A2.
XX
XX 10-JAN-2002.
PD
XX
XX 03-JUL-2001; 2001WO-IB001445.
PF
XX
XX 03-JUL-2000; 2000GB-00016363.
PR 11-JUL-2000; 2000GB-00017047.
PR 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
PR 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
PR 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
PR
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX Ratti G, Grandi G;
PI
XX
XX WPI; 2002-154726/20.
DR
XX
XX N-PSDB; ABL91237.
DR
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
PT
XX
XX Claim 1; Page 93; 364pp; English.
PS
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed Chlamydia pneumoniae protein of the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
CC
XX
XX Sequence 357 AA;
SQ
Query Match 100.0%; Score 31; DB 5; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYAR 6
Db 135 FSRYAR 140

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```

RESULT 16
ABB90579
ID ABB90579 standard; protein; 357 AA.
XX
XX ABB90579;
AC
XX 29-AUG-2003 (revised)
DT 29-JUL-2002 (first entry)
XX
XX
DE Chlamydia pneumoniae CP7224 protein, SEQ ID NO:107.
XX
XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KM human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
XX

```

```

RESULT 17
ABU27032
ID ABU27032 standard; protein; 357 AA.
XX
XX ABU27032;
AC
XX 23-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #12559.
DE
XX

```


KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Chlamydia pneumoniae.
 OS
 XX WO200277183-A2.
 PN
 XX 03-OCT-2002.
 PD
 XX 21-MAR-2002; 2002WO-US009107.
 PF
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948893.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH,
 XX
 DR WPI; 2003-029926/02.
 XX N-PSDB; ACAA30902.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS
 XX Claim 25; SEQ ID NO 54956; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC parent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_ptc_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 357 AA;
 Query Match 100.0%; Score 31; DB 6; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 |||||
 DB 135 FSRYAR 140

RESULT 18
 AEC95703
 ID AEC95703 standard; protein; 357 AA.
 XX
 AC AEC95703;
 XX
 DT 17-NOV-2005 (first entry)
 XX
 DE C. pneumoniae Murg peptidoglycan transferase protein (Cpn 0904).
 XX
 KM diagnosis; autotransporter antigen; antibacterial; vaccine;
 KM Murg peptidoglycan transferase protein; Cpn 0904.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN WO2005084306-A2.
 XX
 PD 15-SEP-2005.
 XX
 PF 02-MAR-2005; 2005WO-US006588.
 XX
 PR 02-MAR-2004; 2004US-0549832P.
 PR 12-JAN-2005; 2005US-0643110P.
 PR 19-JAN-2005; 2005US-0644552P.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 XX
 PI Grandi G, Giulio R;
 XX
 DR WPI; 2005-619258/63.
 DR GENBANK; AAD19042.1.
 XX
 PT New Chlamydia pneumoniae autotransporter protein, useful as an
 PT autotransporter antigen, for raising a specific immune response or for
 PT preventing or treating C. pneumoniae infections in individuals.
 XX
 PS Disclosure; SEQ ID NO 18; 159pp; English.
 XX
 CC The invention relates to a polypeptide for use as an autotransporter
 CC antigen. Also provided is a method of eliciting an immune response in an
 CC individual which involves administering to the individual an Chlamydia
 CC pneumoniae autotransporter protein selected from Cpn0794, Cpn0795,
 CC Cpn0796, Cpn0797, Cpn0798, or Cpn0799 or an immunogenic fragment. The
 CC polypeptide is secreted into the cytoplasm of the host cell through a
 CC Type V autotransporter secretion system mechanism. The polypeptide is
 CC useful as an antigen for raising a C. pneumoniae specific immune
 CC response. It is also useful for raising a systemic immune response in an
 CC individual infected with C. pneumoniae. The polypeptide is also useful in
 CC diagnosis. It can also be used in the preparation of a medicament for the
 CC prevention or treatment of a C. pneumoniae infection in an individual, or
 CC in the preparation of an assay for the diagnosis of a C. pneumoniae
 CC infection in an individual. It can also be used as an autotransporter
 CC protein which immunoreacts with seropositive serum of an individual
 CC infected with C. pneumoniae. The present sequence represents a C.
 CC pneumoniae Murg peptidoglycan transferase protein (Cpn 0904).
 CC
 XX
 SQ Sequence 357 AA;
 Query Match 100.0%; Score 31; DB 9; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 |||||
 DB 135 FSRYAR 140
 RESULT 19
 ADS44828
 ID ADS44828 standard; protein; 463 AA.
 XX
 AC ADS44828;

DT	02-DEC-2004	(first entry)
DE	Bacterial polypeptide #23258.	
KW	Recombinant DNA construct; transformed plant; improved plant property;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;	
KW	pathogen tolerance; pest tolerance; plant disease resistance;	
KW	cell cycle pathway modification; plant growth regulator;	
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;	
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;	
KW	bacterial polypeptide.	
XX	Bacteria.	
XX	US2003233675-A1.	
PN	18-DEC-2003.	
XX	20-FEB-2003; 2003US-00369493.	
PF	21-FEB-2002; 2002US-0360039P.	
PR	(CAOY/) CAO Y.	
PA	(HINK/) HINKLE G J.	
PA	(SLAT/) SLATER S C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B S.	
XX	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;	
PI	WPI; 2004-061375/06.	
XX	New recombinant DNA construct comprising a promoter positioned to provide	
PT	for expression of a polynucleotide encoding a polypeptide from a	
PT	microbial source, useful for producing plants with improved properties.	
PS	Claim 1; SEQ ID NO 23258; 122pp; English.	
XX	The invention relates to a recombinant DNA construct comprising a	
CC	promoter functional in a plant cell, where the promoter is positioned to	
CC	provide for expression of a polynucleotide encoding a polypeptide from a	
CC	microbial source. The invention also relates to a transformed plant	
CC	comprising the recombinant DNA construct and a method of producing a	
CC	transformed plant having an improved property. The plant is a crop plant	
CC	such as maize or soybean. The method of producing a transformed plant	
CC	having an improved property comprises transforming a plant with the	
CC	recombinant DNA construct and growing the transformed plant, where the	
CC	polynucleotide or polypeptide is useful for improving plant properties.	
CC	The recombinant DNA construct is useful for producing plants with	
CC	improved plant properties, e.g. improved cold, heat or drought tolerance,	
CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests,	
CC	increased resistance to plant disease, better growth rate by modification	
CC	of the cell cycle pathway with plant growth regulators, increased rate of	
CC	homologous recombination, modified seed oil or protein yield and/or	
CC	content, improved yield by modification of carbohydrate, nitrogen or	
CC	phosphorus use and/or uptake, by modification of photosynthesis or by	
CC	providing improved plant growth and development under at least one stress	
CC	condition, improved lignin production or improved galactomannan	
CC	production. This sequence represents a bacterial polypeptide used in the	
CC	scope of the invention. Note: The sequence data for this patent did not	
CC	form part of the printed specification but was obtained in electronic	
CC	format from USPTO at seqdata.uspto.gov/sequence.html .	
XX	Sequence 463 AA;	
QY	Query Match 100.0%; Score 31; DB 8; Length 463;	
DB	Best Local Similarity 100.0%; Pred. No. 1-7e+02;	
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
	1 FSRVAR 6	
	76 FSRVAR 81	

RESULT	20	
AAE23630	standard; protein; 466 AA.	
XX		
AC	AAE23630;	
XX		
DT	27-ANG-2002 (first entry)	
XX		
DE	Escherichia coli 6-phospho-strand-glucosidase #	
XX	Secondary structural element; genome-sized data	
KM	6-phospho-strand-glucosidase.	
XX		
OS	Escherichia coli.	
XX		
FH	Key	
FT	Region	Location/Qualifiers
FT		9..11
FT		/note="Strand A"
FT		12..103
FT	Region	/note="UG dipeptide parse"
FT		14..20
FT	Region	/note="Strand B"
FT		48..59
FT	Region	/note="Parse region"
FT		49..51
FT	Region	/note="Strand A"
FT		50..54
FT	Region	/note="Parsing string (PGDSG)"
FT		53..60
FT	Region	/note="Strand B"
FT		62..63
FT	Region	/note="GG dipeptide parse"
FT		71..81
FT	Region	/note="Parse region"
FT		72..84
FT	Region	/note="Helix 1"
FT		73..78
FT	Region	/note="Beta strand"
FT		89..93
FT	Region	/note="Strand C"
FT		95..107
FT	Region	/note="Helix 1"
FT		95..102
FT	Active-site	/note="Active site a"
FT		111..115
FT	Region	/note="Strand C"
FT		116..130
FT	Region	/note="Helix 2"
FT		117..125
FT	Active-site	/note="Active site a"
FT		136..140
FT	Region	/note="Strand D"
FT		138..153
FT	Region	/note="Helix 2"
FT		141
FT	Active-site	/note="Active site b"
FT		158..177
FT	Region	/note="Helix 3"
FT		159..163
FT	Region	/note="Strand D"
FT		164..166
FT	Active-site	/note="Active site b"
FT		181..198
FT	Region	/note="Helix 3"
FT		182..185
FT	Region	/note="Strand E"
FT		184..187
FT	Active-site	/note="Active site c"
FT		205..209
FT	Active-site	/note="Active site c"
FT		205..208
FT	Region	

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FT      Active-site      /note= "Strand E"
PD      207. .209
XX      /note= "Active site c"
FT      212. .226
XX      /note= "Helix 4"
FT      212. .215
XX      /note= "Beta strand"
FT      219. .221
XX      /note= "Beta strand"
FT      242. .245
XX      /note= "Strand X"
FT      248. .268
XX      /note= "Helix 4"
FT      259. .273
XX      /note= "Helix X"
FT      275. .280
XX      /note= "Strand Y"
FT      286. .293
XX      /note= "Helix 5"
FT      318. .320
XX      /note= "Strand Y"
FT      323. .327
XX      /note= "Strand F"
FT      329. .339
XX      /note= "Helix Y"
FT      332. .342
XX      /note= "Helix 5"
FT      375. .382
XX      /note= "Strand Z"
FT      381. .388
XX      /note= "Strand F"
FT      385. .398
XX      /note= "Helix 6"
FT      404. .407
XX      /note= "Strand G"
FT      408. .410
XX      /note= "Active site d"
FT      431. .448
XX      /note= "Helix 7"
FT      446. .452
XX      /note= "Strand Z"
FT      450. .454
XX      /note= "Strand H"
FT      456. .469
XX      /note= "Helix 6"
FT      456. .459
XX      /note= "Strand I"
FT      460. .462
XX      /note= "Dipeptide GP parse"
FT      464. .467
XX      /note= "Strand J"
FT      476. .479
XX      /note= "Strand G"
FT      478. .482
XX      /note= "Strand K"
FT      480. .482
XX      /note= "Active site d"
FT      496. .509
XX      /note= "Helix 8"
FT      497. .517
XX      /note= "Helix 7"
FT      521. .525
XX      /note= "Strand H"
FT      527. .530
XX      /note= "Strand I"
FT      535. .539
XX      /note= "Strand J"
FT      548. .554
XX      /note= "Strand K"
FT      563. .576
XX      /note= "Helix 8"
FN      US6377893-B1.

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XX      23-APR-2002.
PD      19-AUG-1997; 97US-00914375.
XX      25-MAR-1992; 92US-00857224.
XX      (BENN/) BENNER S A.
XX      Benner SA;
XX      WPI; 2002-424771/45.
XX      Methods for excluding or detecting homology between protein families,
XX      useful e.g. for identifying in vitro properties of proteins important for
XX      physiological activity.
XX      Example 5; Col 147-150; 99pp; English.
XX      The invention relates to a method for excluding homology between two
XX      protein families. The method involves constructing models for secondary
XX      structural elements for each family; aligning secondary structural
XX      elements of one family with the secondary structural elements from the
XX      other family around sequence motifs; determining whether secondary
XX      structural elements flanking the sequence motifs in one family are
XX      congruent to secondary structural elements in the other family, so as to
XX      determine if the families are related by common ancestry or not. The
XX      method is used to confirm/deny the hypothesis that proteins are
XX      homologous and related methods are used to identify mutations during
XX      divergent evolution of proteins, to identify in vitro properties of
XX      proteins that are important for physiological activity and to generate
XX      genome-sized databases. The present sequence is Escherichia coli 6-
XX      phospho-strand-glucosidase (EC 3.2.1.86). This sequence is used in the
XX      exemplification of the invention
XX      Sequence 466 AA:
XX      SQ
XX      Query Match 100.0%; Score 31; DB 5; Length 466;
XX      Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
XX      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 FSRYAR 6
Db      154 FSRYAR 159
RESULT 21
AAU34677
ID      AU34677 standard; protein. 474 AA.
XX      AC      AU34677;
XX      DT      14-FEB-2002 (first entry)
XX      DE      E. coli cellular proliferation protein #258.
XX      KW      Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX      antibiotic; drug design.
XX      OS      Escherichia coli.
XX      PN      WO200170955-A2.
XX      PD      27-SEP-2001.
XX      PF      21-MAR-2001; 2001WO-US009180.
XX      PR      21-MAR-2000; 2000US-0191078P.
XX      PR      23-MAY-2000; 2000US-0206848P.
XX      PR      26-MAY-2000; 2000US-0207727P.
XX      PR      23-OCT-2000; 2000US-0242578P.
XX      PR      27-NOV-2000; 2000US-0253625P.
XX      PR      22-DEC-2000; 2000US-0257931P.

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PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELITR-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
DR N-PSDB; AAS553536.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 10270; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC *coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC [tcp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
XX
SQ Sequence 474 AA;
Query Match 100.0%; Score 31; DB 4; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 FSRYYR 6
Db 157 FSRYYR 162
RESULT 22
ADS45088
ID ADS45088 standard; protein; 474 AA.
XX
AC ADS45088;
XX
XX 02-DEC-2004 (first entry)
DT
XX
DE Bacterial polypeptide #23518.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polypeptide.
XX
OS Bacteria.
XX
XX US200323675-A1.
PN
XX
PD 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
PF
XX
PR 21-FEB-2002; 2002US-0360039P.
XX

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 23518; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 474 AA;
Query Match 100.0%; Score 31; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 FSRYYR 6
Db 157 FSRYYR 162
RESULT 23
ABO74595
ID ABO74595 standard; protein; 509 AA.
XX
XX ABO74595;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
DE *Pseudomonas aeruginosa* polypeptide #6770.
XX
XX Bacterial infection; *Pseudomonas aeruginosa* infection; antibacterial.
KM
XX
XX *Pseudomonas aeruginosa*.
OS
XX
XX US6551795-B1.
PN
XX
PD 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
PF
XX
PR 18-FEB-1998; 98US-0074788P.
XX

PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
DR N-PSDB; ABD08166.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 23341; 455PP; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 509 AA;
OY
Query Match 100.0%; Score 31; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 FSRYAR 6
|||
Db 270 FSRYAR 275
RESULT 24
ABG24444
ID ABG24444 standard; protein; 1225 AA.
XX
AC ABG24444;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #24435.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS88631.
PT

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 54803; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1225 AA;
OY
Query Match 100.0%; Score 31; DB 4; Length 1225;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 FSRYAR 6
|||
Db 613 FSRYAR 618
RESULT 25
ABG24819
ID ABG24819 standard; protein; 1258 AA.
XX
AC ABG24819;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #24810.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS89006.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX
PS Claim 20; SEQ ID NO 55178; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1258 AA;

Query Match 100.0%; Score 31; DB 4; Length 1258;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYAR 6
|:|:|:|
Db 1199 FSRYAR 1204

RESULT 26
AAU60688
ID AAU60688 standard; protein: 58 AA.
XX
XX AAU60688;
XX
XX 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #21584.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KM dermatological; osteopathic; neuroprotectant.
XX
XX OS Propionibacterium acnes.
XX
XX PN WO200181581-A2.
XX
XX PD 01-NOV-2001.
XX
XX PF 20-APR-2001; 2001WO-US012865.
XX
XX PR 21-APR-2000; 2000US-0199047P.
XX PR 02-JUN-2000; 2000US-0208841P.
XX PR 07-JUL-2000; 2000US-0216747P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhactia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
XX DR N-PSDB; AAS59612.

XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX
PS Example 1; SEQ ID NO 21883; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 58 AA;

Query Match 90.3%; Score 28; DB 4; Length 58;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYAR 6
|:|:|:|
Db 14 FARYAR 19

RESULT 27
ABM57207
ID ABM57207 standard; protein: 58 AA.
XX
XX ABM57207;
XX
XX 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #21883.
XX
XX Acne vulgaris; antiseporoetic; dermatological; antibacterial;
KM immunostimulant; immune response; vaccine.
XX
XX OS Propionibacterium acnes.
XX
XX PN WO2003033515-A1.
XX
XX PD 24-APR-2003.
XX
XX PF 11-OCT-2002; 2002WO-US032727.
XX
XX PR 15-OCT-2001; 2001US-00978825.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhactia A, Maisonneuve JL;
XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX PI Barth B, Vailieve-Douglas J;
XX WPI; 2003-381789/36.
XX DR N-PSDB; ACF64541.
XX
XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,

PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 21883; 1481bp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 58 AA;
 SQ
 QY Query Match 90.3%; Score 28; DB 6; Length 58;
 Db Best Local Similarity 83.3%; Pred. No. 95; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;
 1 FSRYAR 6
 14 FARYAR 19
 RESULT 28
 AAY12203
 ID AAY12203 standard; protein; 85 AA.
 XX
 AC AAY12203;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Human 5' EST secreted protein SEQ ID NO: 516.
 XX
 KW Human, secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition.
 KW
 OS Homo sapiens.
 XX
 PN WO9906554-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-IB001238.
 XX
 PR 01-AUG-1997; 97US-00905134.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Lacroix B;

XX
 DR WPI; 1999-153784/13.
 DR N-PSDB; AAX41036.
 XX
 PT New nucleic acids encoding human secreted proteins - obtained from cDNA
 PT libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle
 PT and heart tissue.
 XX
 PS Claim 34; Page 585; 622pp; English.
 XX
 CC AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY01602 and
 CC AAY11994 to AAY12260, respectively. The proteins given represent the
 CC signal peptide and an N-terminal fragment of a secreted protein. The
 CC nucleic acid sequences can be used for producing secreted human gene
 CC products. They can also be used to develop products for diagnosis and
 CC therapy. The proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell
 CC
 XX Sequence 85 AA;
 SQ
 QY Query Match 90.3%; Score 28; DB 2; Length 85;
 Db Best Local Similarity 83.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;
 1 FSRYAR 6
 69 FARYAR 74
 RESULT 29
 ABR40679
 ID ABR40679 standard; protein; 90 AA.
 XX
 AC ABR40679;
 XX
 DT 16-MAY-2003 (first entry)
 XX
 DE Oryza sativa oil trait related protein sequence SEQ ID NO:178.
 XX
 KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
 KW receptor-like protein kinase; mitogen activated protein kinase; oil;
 KW lipid-like transcription factor caleosin; ATP citrate lyase; SNF1;
 KW CKC-like transcription factor; antisense inhibition; co-suppression;
 KW transgenic plant.
 KW
 OS Oryza sativa.
 XX
 PN WO2003002751-A2.
 XX
 PD 09-JAN-2003.
 XX
 PF 27-JUN-2002; 2002WO-US020152.
 XX
 PR 29-JUN-2001; 2001US-0301913P.
 XX
 PA (DHPO) DU PONT DE NEMOURS & CO E I.
 PA (PTON-) PTONEER HI-BRED INT INC.
 XX
 PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
 PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 PI Tarczyński WC;
 XX
 DR WPI; 2003-201509/19.

PR	30-MAY-1997;	97US-0048096P.
PR	30-MAY-1997;	97US-0048099P.
PR	30-MAY-1997;	97US-0048131P.
PR	30-MAY-1997;	97US-0048135P.
PR	30-MAY-1997;	97US-0048154P.
PR	30-MAY-1997;	97US-0048160P.
PR	30-MAY-1997;	97US-0048166P.
PR	30-MAY-1997;	97US-0048187P.
PR	30-MAY-1997;	97US-0048188P.
PR	30-MAY-1997;	97US-0048351P.
PR	30-MAY-1997;	97US-0048352P.
PR	30-MAY-1997;	97US-0048355P.
PR	30-MAY-1997;	97US-0050937P.
PR	05-AUG-1997;	97US-0054804P.
PR	19-AUG-1997;	97US-0056370P.
PR	02-OCT-1997;	97US-0060862P.
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Duan R, Hu J,	
PI	Florence KA, Olsen HS, Edner R, Brewer LA, Moore PA, Shi Y,	
PI	Lafleur DM, Ni J;	
XX		
DR	WPI; 1999-070066/06.	
DR	N-PSDB; AAX00705.	
PT	New isolated human genes and the secreted polypeptides they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 11; Page 329; 385pp; English.	
XX		
CC	This sequence represents a secreted human protein encoded by the gene	
CC	clone detailed in the descriptor line. The gene can be used to generate	
CC	fusion proteins by linking to the gene to a human immunoglobulin Fc	
CC	portion (e.g. AAX00602) for increasing the stability of the fused protein	
CC	as compared to the human protein only. The invention relates to 87 novel	
CC	genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino	
CC	acid sequences AAM67807-W68004) which are useful for preventing, treating	
CC	or ameliorating medical conditions e.g. by protein or gene therapy. Also,	
CC	pathological conditions can be diagnosed by determining the amount of the	
CC	new polypeptides in a sample or by determining the presence of mutations	
CC	in the new polynucleotides. Specific uses are described for each of the	
CC	87 polynucleotides, based on which tissues they are most highly expressed	
CC	in (see AAX00611 for described uses)	
XX		
SQ	Sequence 139 AA;	
Query Match	90.3%;	Score 28; DB 2; Length 139;
Best Local Similarity	83.3%;	Pred. No. 2.3e+02;
Matches 5; Conservative	1;	Mismatches 0; Indels 0; Gaps 0;
Oy	1 ESRVAR 6	
Dd	69 FARYAR 74	
RESULT 32		
AADB06538		
ID	AADB06538 standard; protein; 145 AA.	
XX		
AC	AADB06538;	
XX		
DT	20-NOV-2003 (first entry)	
DE	Allioiococcus oclis antigenic protein SEQ ID NO:478.	
XX		
KW	Allioiococcus oclidis; antigenic protein; immunogenic; immunisation;	
KW	gene therapy; Gram-positive bacterium; infection.	
OS	Allioiococcus oclis.	
PN	WO2003048304-A2.	

[illegible]

PN		XX	WO2003048304-A2.
NN		XX	
PD		XX	12-JUN-2003.
PP		XX	
PF		XX	25-NOV-2002; 2002MO-US036123.
PK		XX	
PL		XX	29-NOV-2001; 2001US-033777P.
PR		XX	18-NOV-2002; 2002US-0426742P.
PS		XX	(AMHP) WYETH HOLDINGS CORP.
PT		XX	Fletcher ID, Mcmichael JC, Russell DP, Zagursky RJ;
DR		XX	WPI; 2003-505284/47.
N-PSDB;		XX	AJB06539.
PT		XX	New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
PT		XX	
Claim 33;		XX	SEQ ID NO 480; 1019pp; English.
CC		XX	The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
CC		XX	Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
CC		XX	An isolated polypeptide that is encoded by the polynucleotide (1); (2) an expression vector comprising the novel isolated polynucleotide (1), its complement, degenerate variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2);
CC		XX	(4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polynucleotide that is comprised in the expression vector; (6) a pharmaceutical composition comprising the polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) immunizing against Alloiococcus otitidis by administering to a host the immunogenetic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (10) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, or the antibody of (4), and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polypeptide from the culture. (1) can be used in gene therapy. The CC polynucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
CC		XX	The polynucleotides are useful for expressing and detecting Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis antigen protein from the present invention.
SQ		XX	Sequence 172 AA;
Query Match			90.3%; Score 28; DB 6; Length 172;
Best Local Similarity			83.3%; Pred. No. 2.9e+02;
Matches			5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy			1 FSRVAR 6 :
Dz			149 FSRYSR 154
RESULT 34			
AAW67842			standard; protein; 174 AA.
AC			AAW67842;
DT			25-MAR-1999 (first entry)
DE			Human secreted protein encoded by gene 36 clone HODCU36.
KW			Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW		developmental abnormality; foetal deficiency; blood; allergy; renal;
KM		immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KM		inflammation; ischemic shock; Alzheimer's disease; resectosis; AIDS;
KM		cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW		osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW		endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX		
OS	Homo sapiens.	
PN	MO9842738-A1.	
XX		
PD	01-OCT-1998.	
XX		
PF	19-MAR-1998;	98WO-USO05311.
XX		
PR	21-MAR-1997;	97US-0041276P.
PR	21-MAR-1997;	97US-0041277P.
PR	21-MAR-1997;	97US-0041281P.
PR	21-MAR-1997;	97US-0042344P.
PR	30-MAY-1997;	97US-0048063P.
PR	30-MAY-1997;	97US-0048094P.
PR	30-MAY-1997;	97US-0048095P.
PR	30-MAY-1997;	97US-0048096P.
PR	30-MAY-1997;	97US-0048099P.
PR	30-MAY-1997;	97US-0048131P.
PR	30-MAY-1997;	97US-0048135P.
PR	30-MAY-1997;	97US-0048154P.
PR	30-MAY-1997;	97US-0048160P.
PR	30-MAY-1997;	97US-0048166P.
PR	30-MAY-1997;	97US-0048187P.
PR	30-MAY-1997;	97US-0048188P.
PR	30-MAY-1997;	97US-0048351P.
PR	30-MAY-1997;	97US-0048352P.
PR	30-MAY-1997;	97US-0048355P.
PR	30-MAY-1997;	97US-0050937P.
PR	05-AUG-1997;	97US-0054804P.
PR	19-AUG-1997;	97US-0056370P.
PR	02-OCT-1997;	97US-0060862P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
P1	Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Duan R, Hu J;	
P1	Florence KA, Olsen HS, Edner R, Brewer LA, Moore PA, Shi Y;	
P1	Lafleur DW, Ni Y;	
XX		
DR	WPI: 1999-070066/06.	
XX	N-PsDB; AAX00646.	
XX		
PT	New isolated human genes and the secreted polypeptides they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 11, Page 291, 385PP, English.	
XX		
CC	This sequence represents a secreted human protein encoded by the gene	
CC	clone detailed in the descriptor line. The gene can be used to generate	
CC	fusion proteins by linking to the gene to a human immunoglobulin Fc	
CC	portion (e.g. AAX00602) for increasing the stability of the fused protein	
CC	as compared to the human protein only. The invention relates to 87 novel	
CC	genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino	
CC	acid sequences AW67807-W68004) which are useful for preventing, treating	
CC	or ameliorating medical conditions e.g. by protein or gene therapy. Also,	
CC	pathological conditions can be diagnosed by determining the amount of the	
CC	new polypeptides in a sample or by determining the presence of mutations	
CC	in the new polynucleotides. Specific uses are described for each of the	
CC	87 polynucleotides, based on which tissues they are most highly expressed	
CC	in (see AAX00611 for described uses)	
XX		
SQ	Sequence 174 AA:	
Query Match	90.3%;	Score 28; DB 2; Length 174;
Best Local Similarity	83.3%;	Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		

OY 1 FSRYAR 6
|:||||
XX
Db 69 FARYAR 74

RESULT 35

ADY14896
ID ADY14896 standard; protein; 174 AA.

AC ADY14896;

DT 05-MAY-2005 (first entry)

DE PRO polypeptide SEQ ID NO 702.

XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antineuro;
KW Antitumor; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Vitucide; Gastrointestinal-Gen.; Antipsoriatic; Antisthmatic;
XX Antiallergic; ds; gene; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

PF 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

DR WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT creating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX

PS Claim 8; SEQ ID NO 702; 158bp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX

XX Sequence 174 AA;

Query Match 90.3%; Score 28; DB 9; Length 174;

Best Local Similarity 83.3%; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
|:||||
XX
Db 69 FARYAR 74

RESULT 36
AEF69875
ID AEF69875 standard; protein; 174 AA.

XX AEF69875;

DT 06-APR-2006 (first entry)

DE Microsatellite instability colorectal tumor marker protein SEQ ID NO:53.
XX satellite DNA, tumor marker; therapeutic; diagnosis; prognosis;
KW

KW colorectal tumor; cancer; neoplasm; cytostatic.

XX Homo sapiens.

XX WO2006015047-A2.

XX 09-FEB-2006.

XX 27-JUL-2005; 2005WO-US026647.

XX 28-JUL-2004; 2004US-0591969P.

XX 13-APR-2005; 2005US-00105233.

XX (FARB) BAYER HEALTHCARE LLC.

PI Bugess C, Catino TJ, Molino G, Myerow S, Thiagalingam A;

PI Thibodeau S, Boardman LA, Burgart L, Lewis M;

DR WPI; 2006-155744/16.

DR N-PSDB; AEF69841.

PT Detecting microsatellite instability, useful for monitoring the onset,
PT progression, or regression of cancer, comprises measuring the expression
PT of genes.

PS Claim 24; SEQ ID NO 53; 282bp; English.

XX The invention relates to a method for monitoring the onset, progression,
CC or regression of cancer or a pre-malignant condition, particularly
CC colorectal cancer, in an individual, comprising detecting microsatellite
CC instability in an individual by measuring the expression of the sequence
CC of one or more nucleotide sequences defined in the specification, where
CC microsatellite instability is determined as overexpression of the
CC sequence by at least 2-fold compared to the expression in an individual
CC known to not have microsatellite instability. Alternatively, the method
CC comprises detecting binding of a ligand to a polypeptide encoded by one
CC or more of the above nucleotide sequences. The methods are useful for
CC detecting microsatellite instability in an individual, for identifying
CC colon tissue having microsatellite instability, for monitoring the onset,
CC progression, or regression of cancer or a pre-malignant condition in a
CC subject, for determining prognosis for cancer or a pre-malignant
CC condition in a subject. The nucleotides and polypeptides are useful for
CC determining the efficacy of a test compound or a therapy for inhibiting
CC cancer in a subject and for selecting a composition and method for inhibiting cancer
CC in a subject. The compound, composition and method are useful for
CC treating cancer. This sequence is a protein encoded by a marker DNA
CC sequence specific for a high degree of microsatellite instability (MSI-H
CC marker) relative to colorectal tumors.
XX

XX Sequence 174 AA;

Query Match 90.3%; Score 28; DB 10; Length 174;

Best Local Similarity 83.3%; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
|:||||
XX
Db 69 FARYAR 74

RESULT 37
AEA17517
ID AEA17517 standard; protein; 243 AA.

XX AEA17517;

DT 28-JUL-2005 (first entry)

DE Thale cress caleosin-related family protein, SEQ ID NO: 122.
XX Apolipoprotein; expression; transgenic plant; pharmaceutical;
XX vascular disease; atherosclerosis; vasotropic; antiarteriosclerotic;
KW

KM caleosin.
 OS Arabidopsis thaliana.
 PN WO2005047455-A2.
 XX
 PD 26-MAY-2005.
 XX
 PF 15-NOV-2004; 2004WO-CA001960.
 XX
 PR 14-NOV-2003; 2003US-0519606P.
 PR 16-JUN-2004; 2004US-0579733P.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 XX
 PI Moloney MM, Reid A;
 XX
 DR WPI; 2005-372355/38.
 XX
 PT Expressing apolipoprotein in plants which may be used for treating
 PT vascular diseases, comprises introducing a chimeric nucleic acid
 PT construct into a plant cell.
 XX
 PS Disclosure; SEQ ID NO 122; 530pp; English.
 XX
 CC The present invention relates to methods for expressing apolipoprotein in
 CC plants by introducing a chimeric nucleic acid construct into a plant
 CC cell. Specifically, this comprises providing a chimeric nucleic acid
 CC construct comprising a nucleic acid sequence capable of controlling
 CC expression in plant cells; and a sequence encoding an apolipoprotein
 CC polypeptide; introducing the chimeric nucleic acid construct into a plant
 CC cell; and growing the plant cell into a mature plant where the plant
 CC expresses apolipoprotein. Also disclosed is a composition of
 CC substantially pure apolipoprotein obtained from a plant, or substantially
 CC pure oil bodies comprising an apolipoprotein obtained from plants. The
 CC nucleic acid sequence capable of controlling expression is a seed-
 CC preferred or constitutive promoter such as a phaseolin promoter and a
 CC ubiquitin promoter. The chimeric nucleic acid construct additionally
 CC comprises a nucleic acid sequence encoding a stabilizing polypeptide
 CC linked in frame to the sequence encoding apolipoprotein. It is a plant-
 CC specific oil body protein or a thioredoxin (SEQ ID NO: 56). The oil body
 CC protein is selected from caleosin, caleosin, and steroleosin. The non-
 CC plant specific stabilizing polypeptide is a green fluorescent protein
 CC (SEQ ID NO: 57) or a single chain antibody. The single-chain antibody is
 CC capable of facilitating purification of apolipoprotein expressed in seeds
 CC or is capable of specifically associating with an oil body protein.
 CC Alternatively, the single-chain antibody is a single-chain Fv antibody
 CC (SEQ ID NO: 240) capable of associating with the 18 kDa caleosin from A.
 CC thaliana (D9scrV). The pharmaceutical apolipoprotein formulation may be
 CC used to treat vascular diseases, such as atherosclerosis. The present
 CC sequence is a cholesterosin protein sequence.
 XX
 SQ Sequence 243 AA;
 QY
 QY Query Match 90.3%; Score 28; DB 9; Length 243;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 FSRVYAR 6
 159 FSKYAR 164
 RESULT 38
 ABR40670
 ID ABR40670 standard; protein; 244 AA.
 XX
 AC ABR40670;
 XX
 DT 16-MAY-2003 (first entry)
 XX
 DE Zea mays oil trait related protein sequence SEQ ID NO:160.
 XX

KM plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
 KM receptor-like protein kinase; mitogen activated protein kinase; oil;
 KM LIP5-like transcription factor caleosin; ATP citrate lyase; SNF1;
 KM CKC-like transcription factor; antisense inhibition; co-suppression;
 KM transgenic plant.
 XX
 OS Zea mays.
 XX
 PN WO2003002751-A2.
 XX
 PD 09-JAN-2003.
 XX
 PF 27-JUN-2002; 2002WO-US020152.
 XX
 PR 29-JUN-2001; 2001US-0301913P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Allen SM, Allen WB, Caboon RE, Epebaum S, Famodu OO, Harvey LL;
 PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 PI Tarczyński MC;
 XX
 DR WPI; 2003-201509/19.
 DR N-PSDB; ACC00705.
 XX
 PT Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity, caleosin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
 XX
 PS Claim 12; Page 202-203; 542pp; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (I)
 CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
 CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
 CC activated protein (MAP)-kinase activity, LIP5-like transcription factor
 CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
 CC activity and CKC-like transcription factor activity. Also described: (1)
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 244 AA;
 QY
 QY Query Match 90.3%; Score 28; DB 6; Length 244;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 FSRVYAR 6
 163 FSKYAR 168
 RESULT 39
 ADX91903
 ID ADX91903 standard; protein; 256 AA.
 XX
 AC ADX91903;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 54567.
 XX
 KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM

KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomanan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content.
 XX
 XX Unidentified.
 OS
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 XX 05-NOV-2001; 2001US-00985678.
 PR
 XX (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAO/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI
 XX WPI; 2004-180133/17.
 DR
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PT
 XX
 PS Claim 1; SEQ ID NO 54567; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.secdara.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomanan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX
 XX Sequence 256 AA;
 SQ
 QY Query Match 90.3%; Score 28; DB 8; Length 256;
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FSRYAR 6
 ||:||||
 Db 174 FSKYAR 179
 RESULT 40
 ABG07163
 ID ABG07163 standard; protein; 301 AA.
 XX
 XX AC ABG07163;
 XX
 DT 13-FEB-2002 (first entry)

XX
 XX Novel human diagnostic protein #7154.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 KM
 XX Homo sapiens.
 OS
 XX MO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US008631.
 PP
 XX 31-MAR-2000; 2000US-00540217.
 PR
 XX 23-AUG-2000; 2000US-00649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS71350.
 DR
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 XX
 PS Claim 20; SEQ ID NO 37522; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG10377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 XX Sequence 301 AA;
 SQ
 QY Query Match 90.3%; Score 28; DB 4; Length 301;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FSRYAR 6
 ||:||||
 Db 90 FARYAR 95
 RESULT 41
 AEA17523
 ID AEA17523 standard; protein; 301 AA.
 XX
 XX AC AEA17523;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Thale cress caleosin-1 protein, SEQ ID NO: 128.

XX Apolipoprotein; expression; transgenic plant; pharmaceutical;
KM vascular disease; atherosclerosis; vasotropic; antiarteriosclerotic;
XX caleosin.
OS Arabidopsis thaliana.
XX
PN W02005047455-A2.
XX
PD 26-MAY-2005.
XX
PF 15-NOV-2004; 2004WO-CA001960.
XX
PR 14-NOV-2003; 2003US-0519606P.
XX 16-JUN-2004; 2004US-0579733P.
XX (SEMB-) SEMBIOSYS GENETICS INC.
XX
PI Moloney MM, Reid A;
XX
DR WPI; 2005-372355/38.
XX
PT Expressing apolipoprotein in plants which may be used for treating
PT vascular diseases, comprises introducing a chimeric nucleic acid
PT construct into a plant cell.
XX
PS Disclosure; SEQ ID NO 128; 530pp; English.
XX
XX The present invention relates to methods for expressing apolipoprotein in
XX plants by introducing a chimeric nucleic acid construct into a plant
XX cell. Specifically, this comprises providing a chimeric nucleic acid
XX construct comprising a nucleic acid sequence capable of controlling
XX expression in plant cells; and a sequence encoding an apolipoprotein
XX polypeptide; introducing the chimeric nucleic acid construct into a plant
XX cell; and growing the plant cell into a mature plant where the plant
XX expresses apolipoprotein. Also disclosed is a composition of
XX substantially pure apolipoprotein obtained from a plant, or substantially
XX pure oil bodies comprising an apolipoprotein obtained from plants. The
XX nucleic acid sequence capable of controlling expression is a seed-
XX preferred or constitutive promoter such as a phaseolin promoter and a
XX ubiquitin promoter. The chimeric nucleic acid construct additionally
XX comprises a nucleic acid sequence encoding a stabilizing polypeptide
XX linked in frame to the sequence encoding apolipoprotein. It is a plant-
XX specific oil body protein or a thioresdoxin (SEQ ID NO: 56). The oil body
XX protein is selected from oleosin, caleosin, and steroleosin. The non-
XX plant specific stabilizing polypeptide is a green fluorescent protein
XX (SEQ ID NO: 57) or a single chain antibody. The single-chain antibody is
XX capable of facilitating purification of apolipoprotein expressed in seeds
XX or is capable of specifically associating with an oil body protein.
XX Alternatively, the single-chain antibody is a single-chain Fv antibody
XX (SEQ ID NO: 240) capable of associating with the 18 kDa oleosin from A.
XX thaliana (D9scfv). The pharmaceutical apolipoprotein formulation may be
XX used to treat vascular diseases, such as atherosclerosis. The present
XX sequence is a thale cress caleosin protein sequence.
XX
SQ Sequence 301 AA;
XX
Query Match 90.3%; Score 28; DB 9; Length 301;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX Thale cress caleosin-1 protein, SEQ ID NO: 127.
XX
XX Apolipoprotein; expression; transgenic plant; pharmaceutical;
KM vascular disease; atherosclerosis; vasotropic; antiarteriosclerotic;
XX caleosin.
XX
OS Arabidopsis thaliana.
XX
PN W02005047455-A2.
XX
PD 26-MAY-2005.
XX
PF 15-NOV-2004; 2004WO-CA001960.
XX
PR 14-NOV-2003; 2003US-0519606P.
XX 16-JUN-2004; 2004US-0579733P.
XX (SEMB-) SEMBIOSYS GENETICS INC.
XX
PI Moloney MM, Reid A;
XX
DR WPI; 2005-372355/38.
XX
PT Expressing apolipoprotein in plants which may be used for treating
PT vascular diseases, comprises introducing a chimeric nucleic acid
PT construct into a plant cell.
XX
PS Disclosure; SEQ ID NO 127; 530pp; English.
XX
XX The present invention relates to methods for expressing apolipoprotein in
XX plants by introducing a chimeric nucleic acid construct into a plant
XX cell. Specifically, this comprises providing a chimeric nucleic acid
XX construct comprising a nucleic acid sequence capable of controlling
XX expression in plant cells; and a sequence encoding an apolipoprotein
XX polypeptide; introducing the chimeric nucleic acid construct into a plant
XX cell; and growing the plant cell into a mature plant where the plant
XX expresses apolipoprotein. Also disclosed is a composition of
XX substantially pure apolipoprotein obtained from a plant, or substantially
XX pure oil bodies comprising an apolipoprotein obtained from plants. The
XX nucleic acid sequence capable of controlling expression is a seed-
XX preferred or constitutive promoter such as a phaseolin promoter and a
XX ubiquitin promoter. The chimeric nucleic acid construct additionally
XX comprises a nucleic acid sequence encoding a stabilizing polypeptide
XX linked in frame to the sequence encoding apolipoprotein. It is a plant-
XX specific oil body protein or a thioresdoxin (SEQ ID NO: 56). The oil body
XX protein is selected from oleosin, caleosin, and steroleosin. The non-
XX plant specific stabilizing polypeptide is a green fluorescent protein
XX (SEQ ID NO: 57) or a single chain antibody. The single-chain antibody is
XX capable of facilitating purification of apolipoprotein expressed in seeds
XX or is capable of specifically associating with an oil body protein.
XX Alternatively, the single-chain antibody is a single-chain Fv antibody
XX (SEQ ID NO: 240) capable of associating with the 18 kDa oleosin from A.
XX thaliana (D9scfv). The pharmaceutical apolipoprotein formulation may be
XX used to treat vascular diseases, such as atherosclerosis. The present
XX sequence is a thale cress caleosin protein sequence.
XX
SQ Sequence 301 AA;
XX
Query Match 90.3%; Score 28; DB 9; Length 301;
Best Local Similarity 83.3%; Pred. No. 5.2e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 42
ID ABA17522 standard; proteoin; 301 AA.
XX
AC ABA17522;
XX
DT 28-JUL-2005 (first entry)

RESULT 43
ID ABG27724 standard; proteoin; 499 AA.
XX
AC ABG27724;
XX

XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #27715.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US008631.
XX	
PR	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Drmanac RT, Liu C, Tang YT;
XX	
DR	WPI; 2001-639362/73.
DR	N-PSDB; AAS91911.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity.

PS Claim 20, SEQ ID NO 56083; 103pp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probe, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences
SQ Sequence 499 AA;

Query Match	90.3%	Score 28	DB 4	Length 499
Best Local	Similarity 83.3%	Pred. No. 8.7e+02		
Matches 5	Conservative 1	Mismatches 0	Indels 0	Gaps 0

Qy	1	FSRYAR	6
		:	
		:	
		:	
		:	
Db	89	FARYAR	94

RESULT 44	
ABG29681	
ID	ABG29681 standard; protein; 520 AA.
XX	
AC	ABG29681;
XX	
DT	18-FEB-2002 (first entry)

XX	
DE	Novel human diagnostic protein #29672.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US008631.
XX	
PR	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Drimaeac RT, Liu C, Tang YT;
XX	
DR	WPI; 2001-639362/73.
DR	N-PSDB; AAS93868.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity

PS Claim 20, SEQ ID NO 60040; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 520 AA;

Query Match	90.3%	Score 28;	DB 4;	Length 520;
Best Local Similarity	83.3%	Pred. 9e+02;		
Matches 5; Conservative	1;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	FSRRYAR	6
		:	
Db	46	FNRRYAR	51

RESULT	45
ADN18185	
ID	ADN18185 standard; protein; 681 AA
XX	
AC	ADN18185;
XX	
DT	02-DEC-2004 (first entry)
DE	Bacterial polypeptide #838.

XX Recombinant DNA construct: transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polypeptide.
OS Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAO Y.) CAO Y.
XX (HINKLE G J.) HINKLE G J.
XX (SLATER S C.) SLATER S C.
XX (CHEN X.) CHEN X.
XX (GOLDMAN B S.) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 838; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 681 AA;
XX
XX Query Match 90.3%; Score 28; DB 8; Length 681;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 FSRYAR 6
XX | : |||||
XX Db 515 FARYAR 520

ID ABG04036 standard; protein; 847 AA.
XX
XX AC ABG04036;
XX 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #4027.
XX
XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX OS
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/773.
XX N-PSDB; AAS68223.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 20; SEQ ID NO 34395; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_ptc_sequences
XX SQ Sequence 847 AA;
XX
XX Query Match 90.3%; Score 28; DB 4; Length 847;
XX Best Local Similarity 83.3%; Pred. No. 1.5e+03;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 FSRYAR 6
XX | : |||||
XX Db 835 FARYAR 840

AC	ABP76771;
XX	
DT	07-MAR-2003 (first entry)
XX	
DE	N. gonorrhoeae amino acid sequence SEQ ID 72.
XX	
KW	Antibacterial; infection; vaccine; gene therapy.
XX	
OS	Neisseria gonorrhoeae.
XX	
PN	WO200279243-A2.
PD	10-OCT-2002.
XX	
Pf	12-FEB-2002; 2002MO-IB002069.
XX	
PR	12-FEB-2001; 2001GB-00003424.
XX	
PA	(CHIR-) CHIRON SPA.
XX	
PI	Fontana MR, Pizza M, Maignani V, Monaci E;
XX	
DR	WPI; 2003-058415/05.
XX	
PT	New protein from Neisseria gonorrhoeae, useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection.
XX	
PS	Claim 1; Page 182; 815pp; English.
XX	
CC	The present invention relates to proteins from Neisseria gonorrhoeae.
XX	
CC	Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy.
XX	
CC	Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
XX	
SQ	Sequence 1206 AA;
QY	Query Match 90.3%; Score 28; DB 6; Length 1206; Best Local Similarity 83.3%; Pred.No. 2.1e+03; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB	939 FARVAR 944
RESULT 48	
ID	ABP78681 standard; protein; 1206 AA.
XX	
AC	ABP78681;
XX	
DT	07-MAR-2003 (first entry)
XX	
DE	N. gonorrhoeae amino acid sequence SEQ ID 3892.
XX	
KW	Antibacterial; infection; vaccine; gene therapy.
XX	
OS	Neisseria gonorrhoeae.
XX	
PN	WO200279243-A2.
PD	10-OCT-2002.
XX	
Pf	12-FEB-2002; 2002MO-IB002069.
XX	
PR	12-FEB-2001; 2001GB-00003424.
XX	
PA	(CHIR-) CHIRON SPA.

XX	Fontana MR, Pizza M, Maignani V, Monaci E;
PI	
XX	WP1; 2003-058415/05.
DR	N-PSDB; ABZ39651.
XX	
XX	New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT	medicament for treating or preventing N. gonorrhoeae infection.
PS	
XX	Disclosure; Page 470; 815pp; English.
XX	
CC	The present invention relates to proteins from Neisseria gonorrhoeae.
CC	Also disclosed are the nucleic acid molecules encoding the proteins and
CC	antibodies that specifically bind to the proteins. The composition
CC	comprising the protein, nucleic acid or antibody is useful for the
CC	manufacture of a medicament for treating or preventing N. gonorrhoeae
CC	infection, this may be in the form of a vaccine or gene therapy.
CC	Sequences given in records ABP76736-ABP81046 represent nucleic acid
CC	molecules of the invention
XX	
XX	Sequence 1206 AA:
XX	
QY	1 PSRYAR 6
DB	939 FARYAR 944
XX	
XX	Query Match 90.3%; Score 28; DB 6; Length 1206;
XX	Best Local Similarity 83.3%; Pred. No. 2.1e+03;
XX	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
XX	
XX	RESULT 49
XX	ABO69413
XX	ID ABO69413 standard; protein; 1778 AA.
XX	
XX	ABO69413;
XX	
DT	29-JUL-2004 (First entry)
XX	
DE	Pseudomonas aeruginosa polypeptide #1588.
XX	
KW	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX	
OS	Pseudomonas aeruginosa.
XX	
XX	US6551795-B1.
XX	
XX	22-APR-2003.
XX	
XX	18-FEB-1999; 99US-00252991.
XX	
XX	18-FEB-1998; 98US-0074788P.
XX	27-JUL-1998; 98US-0094190P.
XX	
XX	(GENO-) GENOME THERAPEUTICS CORP.
XX	
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX	
XX	WP1; 2003-615309/58.
DR	N-PSDB; ABD02984.
XX	
PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, p-
PT	useful as molecular targets for diagnostics, prophylaxis and treatment of
XX	pathological conditions resulting from bacterial infection.
XX	
PS	Disclosure; SEQ ID NO 18159; 455pp; English.
XX	
CC	The invention relates to Pseudomonas aeruginosa polypeptides and the
CC	polynucleotides encoding them. The sequences are useful in diagnosis and
CC	therapy of pathological conditions, as molecular targets for diagnostics,
CC	prophylaxis and treatment of pathological conditions resulting from a
CC	bacterial infection, for evaluating a compound, such as a polypeptide,
CC	for the ability to bind a P. aeruginosa nucleic acid, as components of

CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences AB067826-
CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1778 AA;

Query March 90.3%; Score 28; DB 7; Length 1778;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYYR 6
|||:|
Db 1131 FSKYAR 1136

RESULT 50
AB878221
ID AB878221 standard; protein; 2151 AA.

AC AB878221;
XX
DT 25-NOV-2002 (first entry)

DE AlphaIC subunit of a voltage-dependent L-type calcium channel.

KM Zebrafish; alphaIC subunit; voltage-dependent L-type calcium channel;
KW heart disease; cardiac arrhythmia; atrial fibrillation.

XX Danio rerio.

OS WO200262204-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003441.

XX 07-FEB-2001; 2001US-0267332P.

XX (GEHO) GEN HOSPITAL CORP.

XX Fishman MC, Rottbauer W;

XX WPI, 2002-643382/69.

DR N-PSDB; ABQ78616.

XX Determining whether a subject has or is at risk of developing disease
PT related to alphaIC subunit of voltage-dependent L-type calcium channel,
PT by detecting mutations in genes encoding the subunit in sample of
PT subject.

XX Disclosure; Page 57-61; 61pp; English.

XX The present sequence represents a zebrafish alphaIC subunit of a voltage-
CC dependent L-type calcium channel. The specification describes a method
CC for determining whether a test subject has or is at risk of developing a
CC disease or condition related to the alphaIC subunit. The method involves
CC analyzing a nucleic acid molecule sample from the test subject to
CC determine whether the test subject has a mutation in a gene encoding the
CC alphaIC subunit, where the presence of a mutation indicates that subject
CC has or is at risk of developing the disease. The method is useful for
CC determining whether a test subject (preferably mammal e.g. human) has, or
CC is at risk of developing, a disease or condition related to the alphaIC,
CC e.g. heart disease including cardiac arrhythmia or atrial fibrillation
SQ Sequence 2151 AA;

Query March 90.3%; Score 28; DB 5; Length 2151;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYYR 6
|||:|
Db 515 FSRYSR 520

Search completed: August 29, 2006, 05:59:43
Job time : 55.2079 secs

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OM protein - protein search, using sw model

Run on: August 29, 2006, 06:00:58 ; Search time 6 Seconds
(without alignments)
96.217 Million cell updates/sec

Title: US-10-541-343-2
Perfect score: 31
Sequence: 1 FSRVAR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR 80: *
1: Dir1: *
2: Dir2: *
3: Dir3: *
4: Dir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	356	2	C64890
2	31	100.0	357	2	C72022
3	31	100.0	357	2	F86603
4	31	100.0	463	2	C69997
5	31	100.0	474	2	H65051
6	31	100.0	474	2	D91075
7	31	100.0	474	2	C85920
8	31	100.0	496	2	B83591
9	28	90.3	339	2	T07092
10	28	90.3	304	2	T16828
11	28	90.3	409	2	A93271
12	28	90.3	437	2	H95857
13	28	90.3	475	2	A95376
14	28	90.3	573	2	D90202
15	28	90.3	681	2	E64908
16	28	90.3	681	2	C90897
17	28	90.3	681	2	D85720
18	28	90.3	877	2	AC2211
19	28	90.3	1746	2	D83181
20	27	87.1	36	2	F84791
21	27	87.1	43	2	A10982
22	27	87.1	108	2	F97521
23	27	87.1	108	2	AH2740
24	27	87.1	208	2	B84920
25	27	87.1	220	2	B49547
26	27	87.1	232	2	UC4755
27	27	87.1	286	2	AE3245
28	27	87.1	286	2	T03434
29	27	87.1	292	2	S35983

30	27	87.1	293	2	E87697	dUDP-4-dehydroxam
31	27	87.1	302	2	T45890	splicing factor-1i
32	27	87.1	341	2	JC5855	polyketide synthas
33	27	87.1	354	2	C83575	fructose-1,6-bisph
34	27	87.1	410	2	E75080	3-phosphoglycerate
35	27	87.1	410	2	D71065	probable phosphogl
36	27	87.1	411	2	T15705	hypothetical prote
37	27	87.1	453	2	D87672	glutamate-cysteine
38	27	87.1	456	2	AH0551	proline-specific p
39	27	87.1	457	2	B64769	proline transport
40	27	87.1	457	2	D90685	proline permease t
41	27	87.1	457	2	H85535	proline permease t
42	27	87.1	463	2	A10388	probable proline-s
43	27	87.1	465	2	C42603	phospho-beta-glucos
44	27	87.1	478	2	C87351	aldehyde dehydroge
45	27	87.1	579	2	B86565	oligopeptide perme
46	27	87.1	579	2	C72059	peptide ABC transp
47	27	87.1	605	2	S16561	glutamine-fructose
48	27	87.1	608	1	S01040	glutamine-fructose
49	27	87.1	608	2	C97575	hypothetical prote
50	27	87.1	608	2	AC2796	hypothetical prote
51	27	87.1	608	2	B95332	Naom Glutamine ami
52	27	87.1	650	2	JC7095	sodium-dependent v
53	27	87.1	661	1	TNBE12	74k alpha trans-in
54	27	87.1	672	2	E70717	hypothetical prote
55	27	87.1	680	2	AH0678	hypothetical prote
56	27	87.1	680	2	A42297	peptidyl-dipeptida
57	27	87.1	1421	2	T00333	hypothetical prote
58	27	87.1	3228	2	T21381	conserved hypotet
59	26	83.9	80	2	H82194	conserved hypotet
60	26	83.9	102	2	S49794	hypothetical prote
61	26	83.9	114	2	C86401	protein T2205.5 [i
62	26	83.9	121	2	H95121	Tn5252, Orf 9 prot
63	26	83.9	174	2	T38839	hypothetical prote
64	26	83.9	231	2	AB3228	gened protein [imp
65	26	83.9	250	2	C90606	hypothetical prote
66	26	83.9	261	2	T32399	hypothetical prote
67	26	83.9	265	2	T32400	hypothetical prote
68	26	83.9	265	2	T35850	probable hydrolase
69	26	83.9	265	2	F86522	Ctl43 hypotnetical
70	26	83.9	268	2	H72101	conserved hypotet
71	26	83.9	287	2	B69148	hypothetical prote
72	26	83.9	297	2	T26464	hypothetical prote
73	26	83.9	322	2	C69528	conserved hypotet
74	26	83.9	325	2	G70771	probable peptidetr
75	26	83.9	331	2	C72015	glycerol-3-phospha
76	26	83.9	331	2	D86610	glycerol-3-P acylt
77	26	83.9	334	2	E90037	conserved hypotet
78	26	83.9	336	2	B84311	histidinol-phospha
79	26	83.9	343	1	A57014	prostatesin (EC 3.4.
80	26	83.9	360	2	T27324	hypothetical prote
81	26	83.9	362	2	C87532	transcription regu
82	26	83.9	431	2	AD1237	arsenic efflux pum
83	26	83.9	454	2	H70158	probable PE protei
84	26	83.9	468	2	E70839	hydroxymethylgluta
85	26	83.9	474	2	T09688	hypothetical prote
86	26	83.9	497	2	D55102	sile-specific DNA-
87	26	83.9	497	2	F97970	zinc metalloprotei
88	26	83.9	509	2	E90071	hypothetical prote
89	26	83.9	520	2	D90014	antA protein - Azo
90	26	83.9	533	2	A44514	hypothetical prote
91	26	83.9	549	2	C70689	ATP-dependent RNA
92	26	83.9	571	2	T25376	SAC2 protein - Yea
93	26	83.9	641	2	S69651	chemotaxis protein
94	26	83.9	654	1	QRECCS	hypothetical prote
95	26	83.9	654	2	B85802	sensory transducer
96	26	83.9	654	2	F90953	probable membrane
97	26	83.9	703	2	AG0242	hypothetical prote
98	26	83.9	727	2	T18665	hypothetical prote
99	26	83.9	763	2	T27937	probable MreB peni
100	26	83.9	781	2	H95392	probable chemotaxi
101	26	83.9	812	2	A71335	alpha-amylase G-6
102	26	83.9	958	2	E83701	

103	26	83.9	1058	2	A48195	ubiquitin-protein
104	26	83.9	1190	2	F86677	pyruvate-flavodoxi
105	26	83.9	1436	2	F86904	conserved hypochet
106	26	83.9	1626	2	T26318	hypothetical prote
107	26	83.9	1664	2	S67250	DNA-directed RNA p
108	26	83.9	1684	2	S10789	amylase A-180 - al
109	25	80.6	75	2	T03192	hypothetical prote
110	25	80.6	106	2	G90356	hypothetical prote
111	25	80.6	109	2	B95124	conserved hypochet
112	25	80.6	110	2	C86735	conserved hypochet
113	25	80.6	120	2	D97994	conserved hypochet
114	25	80.6	135	2	A24916	ribosomal protein
115	25	80.6	141	2	AE1009	probable Zn(II) - re
116	25	80.6	182	2	AG3449	tripartite transpo
117	25	80.6	185	2	H81837	peptidylprolyl iso
118	25	80.6	185	2	H81103	peptidylprolyl iso
119	25	80.6	186	2	T17497	anhydrin repeat pr
120	25	80.6	201	2	G90084	hypothetical prote
121	25	80.6	205	2	F83333	hypothetical prote
122	25	80.6	208	2	B81327	hypothetical prote
123	25	80.6	212	2	T23211	hypothetical prote
124	25	80.6	218	2	J50163	GTP-binding protei
125	25	80.6	219	2	G84723	probable Ras type
126	25	80.6	219	2	S52024	GTP-binding protei
127	25	80.6	219	2	S52646	GTP-binding protei
128	25	80.6	227	2	C97051	RNA polymerase sig
129	25	80.6	236	2	C35620	coenzyme F420 hydr
130	25	80.6	238	2	A72677	hypothetical prote
131	25	80.6	240	2	B71615	YcpB protein, 1st
132	25	80.6	245	2	T04797	embryo-specific pr
133	25	80.6	248	2	S61960	hypothetical prote
134	25	80.6	251	2	T17397	vir10 protein - Dlc
135	25	80.6	257	2	T18969	hypothetical prote
136	25	80.6	270	2	D69791	conserved hypochet
137	25	80.6	293	1	B72325	riboflavin kinase/
138	25	80.6	297	1	PRSMAG	streptogristin A (E
139	25	80.6	304	2	A49185	interphotoreceptor
140	25	80.6	315	2	D72086	conserved hypochet
141	25	80.6	315	2	E86538	CT047 hypothetical
142	25	80.6	343	2	C75260	conserved hypochet
143	25	80.6	352	2	C70532	hypothetical prote
144	25	80.6	359	2	T44332	hypothetical prote
145	25	80.6	360	2	F95933	probable glycosylt
146	25	80.6	362	2	S77767	CTP synthase (EC 6
147	25	80.6	362	2	T51464	RIMC-H2 zinc finge
148	25	80.6	364	2	I45915	interstitial retin
149	25	80.6	384	2	E89088	conserved hypochet
150	25	80.6	398	2	B86298	protein F309.11 (i
151	25	80.6	398	2	T37083	probable transpos
152	25	80.6	411	1	JC5859	polyketide synthas
153	25	80.6	414	2	A29835	Sail protein - Sac
154	25	80.6	430	2	S25977	ribosomal protein
155	25	80.6	436	2	F87557	adenylosuccinate 1
156	25	80.6	436	2	G87756	protein T01A4.3 (i
157	25	80.6	440	2	S49765	Tya protein - yeas
158	25	80.6	440	2	S69970	Tya protein - yeas
159	25	80.6	440	2	S52895	Tya protein - yeas
160	25	80.6	440	2	F64904	hpa protein - Sac
161	25	80.6	465	2	T29443	probable two-compo
162	25	80.6	465	2	AC0438	conserved hypochet
163	25	80.6	470	2	C95055	6-phospho-beta-gal
164	25	80.6	478	2	H97924	6-phospho-beta-gal
165	25	80.6	478	2	T21353	hypothetical prote
166	25	80.6	492	2	H70959	hypothetical prote
167	25	80.6	511	2	A46020	potassium channel
168	25	80.6	511	2	S07095	potassium channel
169	25	80.6	520	2	H83134	4-hydroxyphenylace
170	25	80.6	526	2	T29484	hypothetical prote
171	25	80.6	529	2	H81650	conserved hypochet
172	25	80.6	529	2	D71489	hypothetical prote
173	25	80.6	531	2	H72040	conserved hypochet
174	25	80.6	531	2	G86583	CT632 hypothetical
175	25	80.6	539	2	B72707	hypothetical prote
176	25	80.6	554	2	C82700	CTP synthetase XFI
177	25	80.6	556	2	A69718	squalene-hopene cy
178	25	80.6	585	2	A39395	delayed rectifier
179	25	80.6	642	2	A10263	DNA topoisomerase
180	25	80.6	649	2	AG0710	DNA topoisomerase
181	25	80.6	653	2	A85786	DNA topoisomerase
182	25	80.6	653	2	E90937	DNA topoisomerase
183	25	80.6	653	2	JV0049	DNA topoisomerase
184	25	80.6	672	2	T06560	photomorphogenesis
185	25	80.6	675	2	T01112	photomorphogenesis
186	25	80.6	695	2	T40717	hypothetical prote
187	25	80.6	703	2	T04191	hypothetical prote
188	25	80.6	773	2	AE2553	hypothetical prote
189	25	80.6	776	2	S67053	probable membrane
190	25	80.6	781	2	B64222	DNA topoisomerase
191	25	80.6	789	2	S73357	CT3357
192	25	80.6	831	2	G87620	topoisomerase IV c
193	25	80.6	835	2	S40140	topoisomerase rec
194	25	80.6	837	2	H87638	ribonucleoside-dip
195	25	80.6	840	2	A87639	tonB-dependent rec
196	25	80.6	842	2	AB0674	tonB-dependent rec
197	25	80.6	898	2	A82298	probable hydrolase
198	25	80.6	900	2	JC5234	transaition initia
199	25	80.6	908	2	T22376	methionine-tRNA li
200	25	80.6	923	2	E70820	hypothetical prote
201	25	80.6	925	2	A55748	hypothetical glyci
202	25	80.6	978	2	G75516	protein kinase (EC
203	25	80.6	980	2	T27342	maltooligosyltreha
204	25	80.6	1038	1	WZBE21	hypothetical prote
205	25	80.6	1046	2	T42720	gene 21 protein -
206	25	80.6	1046	2	T42734	cytoplasmic linker
207	25	80.6	1167	2	T06146	cytoplasmic linker
208	25	80.6	1286	1	RJ0BP	disease resistance
209	25	80.6	1307	2	T25563	interphotoreceptor
210	25	80.6	1339	2	A84683	hypothetical prote
211	25	80.6	1392	2	A43336	probable SNF2 subf
212	25	80.6	1427	2	S22635	microtubule-vesicl
213	25	80.6	1592	2	T16055	rescin - human
214	25	80.6	1755	2	S69699	hypothetical prote
215	25	80.6	2133	2	T30637	TYB protein - yeas
216	25	80.6	2191	2	G89779	hypothetical prote
217	25	80.6	2764	2	T13949	hypothetical prote
218	25	80.6	2802	2	T13945	neurofibromin - fir
219	25	80.6	2802	2	T13947	neurofibromin - fir
220	25	80.6	4116	2	T13719	neurofibromin - fir
221	25	80.6	50	2	E71266	calo protein - fru
222	24	77.4	72	2	JC5628	hypothetical prote
223	24	77.4	99	2	T25759	mandibular organ.i
224	24	77.4	107	2	AB3271	hypothetical prote
225	24	77.4	148	2	C82337	hypothetical prote
226	24	77.4	156	2	F91277	hypothetical prote
227	24	77.4	156	2	F68118	hypothetical prote
228	24	77.4	161	2	G75059	hypothetical prote
229	24	77.4	180	2	S60204	hypothetical prote
230	24	77.4	196	2	F97096	trioic protein - co
231	24	77.4	219	2	E90439	ribosomal protein
232	24	77.4	220	2	T24319	conserved hypochet
233	24	77.4	221	2	AB6163	hypothetical prote
234	24	77.4	226	2	G69129	protein F15K9.22 (
235	24	77.4	229	2	AE1300	hypothetical prote
236	24	77.4	229	2	AE1672	ribonuclease III h
237	24	77.4	230	2	F95279	ribonuclease III h
238	24	77.4	253	2	T30928	probable GntR-fam1
239	24	77.4	274	2	T51459	hypothetical prote
240	24	77.4	277	2	S65069	hypothetical prote
241	24	77.4	277	2	AG1037	chitinase (EC 3.2.
242	24	77.4	283	2	B98113	probable capsid pr
243	24	77.4	291	2	T21702	hypothetical prote
244	24	77.4	296	2	I53142	hypothetical prote
245	24	77.4	296	2	A47318	gene Merc protein
246	24	77.4	301	2	C72583	RNA-binding protei
247	24	77.4	315	2	S57696	hypothetical prote
248	24	77.4	323	2	B83464	prohibitin PHB2 -
						flagellar motor sw

249	24	77.4	323	2	B86329	hypothetical prote	322.	24	77.4	889	1	A44153	aconitate hydratase
250	24	77.4	324	2	D64387	hypothetical prote	323.	24	77.4	982	2	T34830	polyketide synthase
251	24	77.4	329	2	A69796	hypothetical prote	324	24	77.4	985	2	S15965	hypothetical prote
252	24	77.4	331	2	A56090	hyaluronoglucuronil	325	24	77.4	1031	2	F83561	probable DNA polym
253	24	77.4	333	2	E95037	carbohydrate kinase	326	24	77.4	1060	2	T43046	retrovirus-related
254	24	77.4	333	2	H97907	2-dehydro-3-deoxyg	327	24	77.4	1062	2	T16507	hypothetical prote
255	24	77.4	336	2	T35215	hypothetical prote	328	24	77.4	1456	1	MMWGPV	RNA-directed RNA p
256	24	77.4	337	2	AD1920	ABC phosphate tran	329	24	77.4	1489	2	G83771	hypothetical prote
257	24	77.4	337	2	H71474	probable peptidogl	330	24	77.4	1638	2	D87749	protein unc-73b [i
258	24	77.4	333	2	G86737	hypothetical prote	331	24	77.4	1846	2	A53289	myr 6, unconvencio
259	24	77.4	367	2	A87092	glutamate 5-kinase	332	24	77.4	2139	2	A44467	voltage-dependent
260	24	77.4	369	2	T50660	glutamate 5-kinase	333	24	77.4	2143	2	JH0427	calcium channel pr
261	24	77.4	376	2	E70680	probable prob - My	334	24	77.4	2166	2	S11339	calcium channel al
262	24	77.4	378	2	F91186	probable membrane	335	24	77.4	2220	2	S05054	calcium channel pr
263	24	77.4	378	2	E86033	probable membrane	336	24	77.4	2488	2	A45290	guanine nucleotide
264	24	77.4	378	2	S47807	hypothetical 41.8k	337	24	77.4	2488	2	T42739	hypothetical prote
265	24	77.4	384	2	H96829	probable RNA-bind	338	24	77.4	3429	2	T13853	protein-tyrosine k
266	24	77.4	390	2	T28967	hypothetical prote	339	23	74.2	57	2	PT0201	DNA-directed RNA p
267	24	77.4	401	2	S62465	probable moltydopt	340	23	74.2	60	2	A84270	hypothetical prote
268	24	77.4	408	2	D70365	fimbrial assembly	341	23	74.2	83	2	T07538	heat shock protein
269	24	77.4	410	2	S68188	phosphoglycerate k	342	23	74.2	88	2	PC4238	heat shock protein
270	24	77.4	413	2	S45467	aminopeptidase y h	343	23	74.2	92	1	S44503	phenol 2-monooxyge
271	24	77.4	447	2	T25264	hypothetical prote	344	23	74.2	94	2	JC1479	heat shock protein
272	24	77.4	459	1	GLAG	beta-glucosidase (345	23	74.2	94	2	A49855	heat shock protein
273	24	77.4	459	1	A13107	beta-glucosidase (346	23	74.2	94	2	A41884	class I heat-shock
274	24	77.4	466	2	C98179	transporth protein	347	23	74.2	94	2	A83720	chaperonin groES -
275	24	77.4	466	2	T44252	hypothetical prote	348	23	74.2	95	2	S72613	Ig heavy chain V r
276	24	77.4	467	2	A75609	hypothetical prote	349	23	74.2	95	2	S20777	S-100 protein p -
277	24	77.4	471	2	D83546	probable amino aci	350	23	74.2	95	2	S24146	hypothetical prote
278	24	77.4	473	2	B95376	probable ArcD2 arg	351	23	74.2	101	2	AF0223	hypothetical prote
279	24	77.4	474	2	H70896	probable fumarate	352	23	74.2	109	2	D97991	hypothetical prote
280	24	77.4	477	2	G70427	biotin carboxylase	353	23	74.2	109	2	G64609	hypothetical prote
281	24	77.4	478	2	G81679	3-dehydroquininate d	354	23	74.2	116	2	C91279	probable growth in
282	24	77.4	478	2	C71523	probable shikimate	355	23	74.2	116	2	D49339	cell growth regula
283	24	77.4	481	2	B97348	hypothetical prote	356	23	74.2	116	2	D86120	Ig heavy chain V r
284	24	77.4	488	2	B87540	hypothetical prote	357	23	74.2	120	2	A44371	hypothetical prote
285	24	77.4	491	2	D70916	hypothetical glyci	358	23	74.2	126	2	B82448	hypothetical prote
286	24	77.4	491	2	AC0133	probable permease	359	23	74.2	131	2	C65089	hypothetical prote
287	24	77.4	499	2	A47751	NADH2 dehydrogenas	360	23	74.2	132	2	AD0108	conserved hypochet
288	24	77.4	503	2	S14275	steroid 6beta-mono	361	23	74.2	134	2	A88691	protein F4H10.9 [
289	24	77.4	503	2	AH3535	periplasmic dipept	362	23	74.2	135	2	T12863	hypothetical prote
290	24	77.4	506	2	T35261	probable metallope	363	23	74.2	135	2	PC4252	hypothetical 135 p
291	24	77.4	508	2	C82138	conserved hypochet	364	23	74.2	140	2	I38855	centromere protein
292	24	77.4	518	2	D84861	probable pectinest	365	23	74.2	140	2	H71903	hypothetical prote
293	24	77.4	523	2	S53401	probable membrane	366	23	74.2	141	2	A83373	hypothetical prote
294	24	77.4	531	2	B83082	probable binding p	367	23	74.2	142	1	S06630	hypoglycemic horm
295	24	77.4	560	1	RGNVPM	trans-activating t	368	23	74.2	146	2	G85756	partial probable m
296	24	77.4	560	2	T10414	immediate early pr	369	23	74.2	152	2	S27150	gene 30.3 protein
297	24	77.4	569	2	AG3132	conserved hypochet	370	23	74.2	163	2	S74604	hypothetical prote
298	24	77.4	569	2	E98155	hypothetical prote	371	23	74.2	164	2	T14187	hypothetical prote
299	24	77.4	582	2	B45878	hypothetical prote	372	23	74.2	164	2	AH2183	hypothetical prote
300	24	77.4	589	2	A71277	arginine-tRNA liga	373	23	74.2	167	2	T28044	nitroreductase fam
301	24	77.4	592	2	T18243	phenylalanine-tRNA	374	23	74.2	167	2	C97091	hypothetical prote
302	24	77.4	599	2	T48383	uracil transporter	375	23	74.2	174	2	B72712	hypothetical prote
303	24	77.4	611	2	A48582	vacuolar ATPase A	376	23	74.2	174	2	I49144	ribonucleoprotein
304	24	77.4	611	2	S56278	DNA-directed DNA p	377	23	74.2	178	2	H64381	cytidylate kinase
305	24	77.4	617	2	T23197	hypothetical prote	378	23	74.2	180	2	A87246	conserved hypochet
306	24	77.4	627	2	AF1074	lytic murein trans	379	23	74.2	180	2	G470912	hypothetical prote
307	24	77.4	631	2	B83404	hypothetical prote	380	23	74.2	182	2	A64007	conserved hypochet
308	24	77.4	643	2	AH0960	cytochrome c-type	381	23	74.2	182	2	AD2914	hypothetical prote
309	24	77.4	643	2	AG0787	cytochrome c-type	382	23	74.2	182	2	G97688	conserved hypochet
310	24	77.4	666	2	E82619	transketolase 1 Xf	383	23	74.2	187	2	E83255	conserved hypochet
311	24	77.4	685	2	F75370	oligopeptidase A -	384	23	74.2	187	2	A99480	hypothetical prote
312	24	77.4	694	2	A95866	probable transketo	385	23	74.2	190	1	A45207	glutathione peroxi
313	24	77.4	707	2	A13290	transketolase (EC	386	23	74.2	194	2	S39798	adenylate kinase (
314	24	77.4	716	2	A75595	hypothetical prote	387	23	74.2	197	2	C81319	hypothetical prote
315	24	77.4	718	2	E71100	hypothetical prote	388	23	74.2	198	2	D75322	conserved hypochet
316	24	77.4	770	2	S60676	cellobiose oxidase	389	23	74.2	208	1	S43851	glutathione transf
317	24	77.4	780	2	T29580	hypothetical prote	390	23	74.2	211	2	A82915	ribosomal protein
318	24	77.4	788	2	B84711	hypothetical prote	391	23	74.2	212	2	G83387	hypothetical prote
319	24	77.4	808	1	P2MCC	2a proteain - compe	392	23	74.2	215	2	T22895	hypothetical prote
320	24	77.4	839	2	AC2637	large atp-dependen	393	23	74.2	216	2	H83998	mutants block spor
321	24	77.4	848	2	B97419	probable ATP-depen	394	23	74.2	217	2	F83840	stage II sporulati

395	23	74.2	218	2	B81906	probable membrane
396	23	74.2	222	2	AC2397	ATP-binding protei
397	23	74.2	224	2	T20553	hypothetical prote
398	23	74.2	230	2	T06309	glutathione peroxi
399	23	74.2	231	2	S34448	small nuclear ribo
400	23	74.2	233	2	S39515	H ⁺ -transporting tw
401	23	74.2	234	2	S09760	hypothetical prote
402	23	74.2	235	2	S46590	uRR3 protein - yea
403	23	74.2	236	2	G84744	probable calcium-b
404	23	74.2	241	2	A49926	transcription regu
405	23	74.2	245	2	I50511	ribonucleoprotein
406	23	74.2	249	2	T10322	proliferating cell
407	23	74.2	251	2	S59314	hypothetical prote
408	23	74.2	252	2	AH0932	thiamin biosynthes
409	23	74.2	252	2	H97189	glycosyltransferas
410	23	74.2	253	2	T36867	hypothetical prote
411	23	74.2	259	2	B64697	UDP-N-acetylenolp
412	23	74.2	259	2	B71823	udp-n-acetylenolp
413	23	74.2	262	2	D82918	conserved hypotet
414	23	74.2	269	2	T32639	hypothetical prote
415	23	74.2	270	2	T40280	26S proteasome reg
416	23	74.2	274	2	G70500	hypothetical prote
417	23	74.2	275	2	F70607	hypothetical prote
418	23	74.2	275	2	T32005	hypothetical prote
419	23	74.2	276	2	G95909	probable 3-deoxy-m
420	23	74.2	280	2	T02004	chitinase (BC 3.2.
421	23	74.2	282	2	AB1929	hypothetical prote
422	23	74.2	285	2	T15498	hypothetical prote
423	23	74.2	285	2	A40657	hypothetical prote
424	23	74.2	288	2	G87342	chemotaxis Mota pr
425	23	74.2	289	2	S54097	Repa protein - Hal
426	23	74.2	291	2	G70605	probable hydrolase
427	23	74.2	293	2	T22385	hypothetical prote
428	23	74.2	294	2	S60991	hypothetical prote
429	23	74.2	294	2	T21668	hypothetical prote
430	23	74.2	295	2	B69514	3-methyladenine DN
431	23	74.2	298	2	D95967	probable transcrip
432	23	74.2	298	2	A75460	conserved hypotet
433	23	74.2	300	2	A84111	sugar transport sy
434	23	74.2	304	2	A83309	hypothetical prote
435	23	74.2	305	2	F71968	hypothetical prote
436	23	74.2	307	2	AG3414	dihydroadipicolinat
437	23	74.2	307	2	T23212	hypothetical prote
438	23	74.2	308	2	AE2359	hypothetical prote
439	23	74.2	309	2	B87457	hypothetical prote
440	23	74.2	310	2	B91247	probable DNA trans
441	23	74.2	310	2	B87667	band 7/Mec-2 famil
442	23	74.2	312	1	S28006	RNA-directed DNA p
443	23	74.2	318	2	T52428	helix-loop-helix p
444	23	74.2	319	2	T37130	probable transport
445	23	74.2	319	2	T36857	conserved hypotet
446	23	74.2	319	2	T46594	phytoene synthase
447	23	74.2	319	2	D90589	hypothetical prote
448	23	74.2	322	2	AF2581	pantothenate kinas
449	23	74.2	323	2	C82234	conserved hypotet
450	23	74.2	323	2	S47966	probable lipid tra
451	23	74.2	325	2	F87049	hypothetical prote
452	23	74.2	327	2	S57121	hypothetical prote
453	23	74.2	328	2	A13511	stomatin like prot
454	23	74.2	329	2	T14760	hypothetical prote
455	23	74.2	330	2	PC4425	lectin-like adhesi
456	23	74.2	333	2	D97363	coaA protein (AE00
457	23	74.2	334	2	AD0775	probable hydrolase
458	23	74.2	334	2	B64977	hypothetical prote
459	23	74.2	334	2	F90991	hypothetical prote
460	23	74.2	334	2	H85836	hypothetical prote
461	23	74.2	338	2	AD0278	probable Lacti-FamI
462	23	74.2	343	1	CES07A	vancomycin resist
463	23	74.2	346	2	A10866	probable oxidoredu
464	23	74.2	346	2	C91090	hypothetical prote
465	23	74.2	346	2	F85935	hypothetical prote
466	23	74.2	346	2	AD0097	probable aldo/keto
467	23	74.2	346	2	T35363	D-alanine-D-alanin

468	23	74.2	346	2	I39077	RNA-binding protei
469	23	74.2	346	2	C65066	hypothetical prote
470	23	74.2	347	2	A85912	hypothetical prote
471	23	74.2	348	2	B70109	translational releas
472	23	74.2	348	2	B83869	hypothetical prote
473	23	74.2	348	2	B96620	protein T30E16.21
474	23	74.2	348	2	I51677	ribonucleoprotein
475	23	74.2	350	2	AH3020	conserved hypotet
476	23	74.2	350	2	A98264	hypothetical 33.7K
477	23	74.2	350	2	JC2116	hippocampal 38k au
478	23	74.2	351	2	D96761	unknown protein f
479	23	74.2	352	2	G65007	hypothetical prote
480	23	74.2	356	1	S55437	translational releas
481	23	74.2	358	2	GA1822	translational releas
482	23	74.2	358	2	G81053	translational releas
483	23	74.2	358	2	H88921	protein F56E10.1 f
484	23	74.2	359	2	T36781	probable gluconate
485	23	74.2	359	2	I38726	FLAV-like neuronal
486	23	74.2	360	1	B32890	translational releas
487	23	74.2	360	1	FCECR1	translational releas
488	23	74.2	360	2	AB0720	peptide chain rele
489	23	74.2	360	2	B83063	peptide chain rele
490	23	74.2	360	2	A85701	peptide chain rele
491	23	74.2	360	2	AC0246	peptide chain rele
492	23	74.2	360	2	D90843	peptide chain rele
493	23	74.2	360	2	JC6057	RNA-binding protei
494	23	74.2	361	1	I64129	translational releas
495	23	74.2	362	2	AB2713	conserved hypotet
496	23	74.2	362	2	H97494	hypothetical prote
497	23	74.2	363	2	AF2375	hypothetical prote
498	23	74.2	366	2	AB2329	translational releas
499	23	74.2	366	2	I51678	ribonucleoprotein
500	23	74.2	367	2	H82016	translational releas

ALIGNMENTS

RESULT 1

probable electron transfer protein - *Escherichia coli* (strain K-12)

C;Species: *Escherichia coli*

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #ext_change 05-Oct-2004

C;Accession: C64890

R;Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi

.A.; Rose, D.J.; Mau, B.; Sha, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MIMD:97426617; PMID:9278503

A;Accession: C64890

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-356 <BLAT>

A;Cross-references: UNIPROT:P76081; UNIPARC:UPI0000131195; GB:AE000236; GB:U00096; NID:gj

C;Superfamily: pithalate dioxigenase reductase; cytochrome-b5 reductase homology; ferredox

C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein; transmembrane

F;116-132/Domain: transmembrane #status predicted <TM01>

F;284-338/Domain: ferredoxin [2Fe-2S] homology <FPR>

F;299,304,307,337/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 100.0%; Score 31; DB 2; Length 356;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYP 6

Db 80 FSRYP 85

RESULT 2

C72022 UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-ac

N/Alternate names: peptidoglycan transferase
C/Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: C72022; E81518
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; PMID:99206606; PMID:10192388
A/Accession: C72022
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <ARN>
A/Cross-references: UNIPROT:Q9Z702; UNIPARC:UPI00000470A7; GB:AE001670; GB:AE001363; NID:
A/Experimental source: strain CML029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gilm, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis Mohn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; PMID:20150255; PMID:10684935
A/Accession: E81518
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <REA>
A/Cross-references: UNIPARC:UPI00000470A7; GB:AE002254; GB:AE002161; NID:97189871; PIND:
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: murG; CP0962
C/Superfamily: murG protein

Query Match 100.0%; Score 31; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
135 FSRYAR 140

DB 135 FSRYAR 140

RESULT 3
F86603
peptidoglycan transferase [imported] - Chlamydomonas pneumoniae (strain J138)
C/Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: F86603
R/Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; IS
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A/Reference number: A86491; PMID:20330349; PMID:10871362
A/Accession: F86603
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <STO>
A/Cross-references: UNIPROT:Q9Z702; UNIPARC:UPI00000470A7; GB:BA000008; NID:98979278; P
A/Experimental source: strain J138
C/Genetics:
A/Gene: murG
C/Superfamily: murG protein

Query Match 100.0%; Score 31; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
135 FSRYAR 140

DB 135 FSRYAR 140

RESULT 4
C69997
probable proline transport protein - Bacillus subtilis
N/Alternate names: probable proline-specific permease
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004

C/Accession: C69997
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berfert
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 380, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
leeh, J.; Harwood, C.R.; Hensat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y., M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A/Authors: Schlitch, D.; Schroeter, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Setor,
akushi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumberg, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; PMID:98044033; PMID:9384377
A/Accession: C69997
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-463 <KUN>
A/Cross-references: UNIPROT:Q34618; UNIPARC:UPI0000060942; GB:Z91119; GB:AL009126; NID:9
A/Experimental source: strain 168
C/Genetics:
A/Gene: ynfA
C/Superfamily: ecotropic retrovirus receptor protein

C/Keywords: amino acid transport; transmembrane protein
F/17-33/Domain: transmembrane #status predicted <TM1>
F/44-60/Domain: transmembrane #status predicted <TM2>
F/97-113/Domain: transmembrane #status predicted <TM3>
F/126-142/Domain: transmembrane #status predicted <TM4>
F/158-174/Domain: transmembrane #status predicted <TM5>
F/203-219/Domain: transmembrane #status predicted <TM6>
F/240-256/Domain: transmembrane #status predicted <TM7>
F/280-296/Domain: transmembrane #status predicted <TM8>
F/336-352/Domain: transmembrane #status predicted <TM9>
F/361-377/Domain: transmembrane #status predicted <TM10>
F/404-420/Domain: transmembrane #status predicted <TM11>
F/428-444/Domain: transmembrane #status predicted <TM12>

Query Match 100.0%; Score 31; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
76 FSRYAR 81

DB 76 FSRYAR 81

RESULT 5
H65051
6-phospho-beta-glucosidase (EC 3.2.1.86) - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: H65051; C44070; S27553
R/Blaetner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; PMID:97426617; PMID:9278503
A/Accession: H65051
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-474 <BLAT>
A/Cross-references: UNIPROT:P24240; UNIPARC:UPI00001260EE; GB:AE000355; GB:U00096; NID:9
A/Experimental source: strain K-12, substrain MG1655
R/Hall, B.G.; Xu, L.
Mol. Biol. Evol. 9, 688-706, 1992
A/Title: Nucleotide sequence, function, activation, and evolution of the cryptic asc oper
A/Reference number: A44070; PMID:92334140; PMID:1630307
A/Accession: C44070
A/Status: preliminary
A/Molecule type: DNA

A;Residues: 1-404,'GT','407-427','C','429-454','HR','457-474<HAL>
A;Cross-references: UNIPARC:UPI000016BE0A; GB:W73326; NID:G145385; PIDN:AAA16430.1; PID:
A;Experimental source: strain LP103
A;Note: sequence extracted from NCBI backbone (NCBIN:109109, NCBI:P.109114)
C;Genetics:
A;Gene: aacB
A;Map position: 59 min
C;Superfamily: Agrobacterium beta-glucosidase
C;Keywords: glycosidase; hydrolase

Query Match 100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||
157 FSRYPAR 162

Db 157 FSRYPAR 162

RESULT 6
D91075
6-phospho-beta-glucosidase [imported] - Escherichia coli (strain O157:H7, substrain RIMC
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91075
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A9629; MUID:21156231; PMID:11258796
A;Accession: D91075
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474<HAV>
A;Cross-references: UNIPROT:Q8X841; UNIPARC:UPI00000D09A4; GB:BA000007; PIDN:BA836995.1;
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
C;Superfamily: Agrobacterium beta-glucosidase

Query Match 100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||
157 FSRYPAR 162

Db 157 FSRYPAR 162

RESULT 7
C85920
6-phospho-beta-glucosidase, cryptic [imported] - Escherichia coli (strain O157:H7, subst
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85920
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoultis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: AB5480; MUID:21074935; PMID:11206551
A;Accession: C85920
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474<STO>
A;Cross-references: UNIPROT:Q8X841; UNIPARC:UPI00000D09A4; GB:AE005174; NID:G12517164; F
C;Genetics:
A;Gene: aecB
C;Superfamily: Agrobacterium beta-glucosidase

Query Match 100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||
157 FSRYPAR 162

Db 157 FSRYPAR 162

RESULT 8
B83591
probable transporter PA0443 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83591
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Watterer, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: B83591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496<STO>
A;Cross-references: UNIPROT:Q91674; UNIPARC:UPI00000C505A; GB:AE04481; GB:AE04091; NID
C;Genetics:
C;Superfamily: Escherichia coli probable transport protein b0511

Query Match 100.0%; Score 31; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||
257 FSRYPAR 262

Db 257 FSRYPAR 262

RESULT 9
T07092
Ca+2-binding EF hand protein homolog PM13 - soybean
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07092
R;Hu, T.F.; Tsai, F.Y.; Heing, Y.I.; Chow, T.Y.
submitted to the EMBL Data Library, May 1997
A;Description: Glycine max mRNA for Ca+2-binding EF-hand protein.
A;Reference number: Z15913
A;Accession: T07092
A;Status: preliminary; translated from GB/EMBL/DDBT
A;Molecule type: mRNA
A;Residues: 1-239<HSU>
A;Cross-references: UNIPROT:Q23959; UNIPARC:UPI00000A8419; EMBL:AF004809; NID:G2270993; I
A;Experimental source: strain Sh1-sh1, cotyledon
C;Genetics:
A;Gene: PM13
C;Superfamily: rice abscisic acid-induced protein

Query Match 90.3%; Score 28; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||
157 FSRYPAR 162

Db 157 FSRYPAR 162

RESULT 10
T16828
hypothetical protein T07F12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16828
R;Chisoe, S.

submitted to the EMBL Data Library, June 1995
 A>Description: The sequence of *C. elegans* cosmid T07F12.
 A/Reference number: Z18585
 A/Accession: T16828
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-304 <CH1>
 A/Cross-references: UNIPROT:Q22323; UNIPARC:UPI000007A68E; EMBL:U29154; NID:9861403; PID
 A/Experimental source: strain Bristol N2
 C/Genetics:
 A/Gene: CESP:T07F12.1
 A/Introns: 34/2; 74/1; 126/1; 165/1; 208/1

Query Match 90.3%; Score 28; DB 2; Length 304;
 Best Local Similarity 83.3%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 Db 147 FARYAR 152

RESULT 11
 A/3271
 probable allantoic permease [imported] - *Brucella melitensis* (strain 16M)
 C/Species: *Brucella melitensis*
 C/Date: 01-Feb-2002 #sequence_rev1sion 01-Feb-2002 #text_change 09-Jul-2004
 C/Accession: AF3271
 R/DeVaccio, V.G.; Kapur, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Loef, T.; Ivanova,
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A/Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A/Reference number: AD3252; PMID:11756688
 A/Accession: AF3271
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-409 <KUR>
 A/Cross-references: UNIPROT:Q8YJDI; UNIPARC:UPI0000057B88; GB:AE08917; PIDD:AAU51337.1;
 A/Experimental source: strain 16M
 C/Genetics:
 A/Gene: BME10155
 A/Map position: 1

Query Match 90.3%; Score 28; DB 2; Length 409;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 Db 176 FSRYAR 181

RESULT 12
 H95857
 probable deaminase protein [imported] - *Sinorhizobium meliloti* (strain 1021) megaplasmid
 C/Species: *Sinorhizobium meliloti*
 C/Date: 24-Aug-2001 #sequence_rev1sion 24-Aug-2001 #text_change 31-Dec-2004
 C/Accession: H95857
 R/Finan, T.M.; Weidner, S.; Wong, K.; Bhurmaster, J.; Chain, P.; Vorholter, F.J.; Hernat
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
 A/Reference number: A95842; MUID:2136508; PMID:11481431
 A/Accession: H95857
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-437 <KUR>
 A/Cross-references: UNIPROT:Q92X34; UNIPARC:UPI00000CB40E; GB:AL591985; PIDD:CA648528.1;
 A/Experimental source: strain 1021, megaplasmid pSymB
 R/Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 J.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
 A/Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Gene: Smb20128
 A/Genome: plasmid
 C/Superfamily: metal-dependent hydrolase (amidohydrolase)

Query Match 90.3%; Score 28; DB 2; Length 437;
 Best Local Similarity 83.3%; Pred. No. 85;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 Db 106 FARYAR 111

RESULT 13
 A/95376
 probable ArcD1 arginine/ornithine antiporter [imported] - *Sinorhizobium meliloti* (strain
 C/Species: *Sinorhizobium meliloti*
 C/Date: 24-Aug-2001 #sequence_rev1sion 24-Aug-2001 #text_change 05-Oct-2004
 C/Accession: A95376
 R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A/Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
 A/Reference number: A95262; MUID:2136509; PMID:11481432
 A/Accession: A95376
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-475 <KUR>
 A/Cross-references: UNIPROT:Q92Y67; UNIPARC:UPI00000CB248; GB:AE006463; PIDD:AA65571.1;
 A/Experimental source: strain 1021, megaplasmid pSymA
 R/Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 J.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
 A/Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Gene: arcD1
 A/Genome: plasmid
 C/Superfamily: ecotropic retrovirus receptor protein

Query Match 90.3%; Score 28; DB 2; Length 475;
 Best Local Similarity 83.3%; Pred. No. 92;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 Db 220 YSRYAR 225

RESULT 14
 D90202
 methionyl-tRNA synthetase (mets) [imported] - *Sulfolobus solfataricus*
 C/Species: *Sulfolobus solfataricus*
 C/Date: 24-May-2001 #sequence_rev1sion 24-May-2001 #text_change 09-Jul-2004
 C/Accession: D90202
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-V
 J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 J.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,

A;Residues: 1-573 <KUR>
 A;Cross-references: UNIPROT:Q9UWM2; UNIPARC:UPI00001365BB; GB:AE006641; NID:G13813723; F
 C;Genetics:
 A;Gene: mets
 C;Superfamily: methionyl-tRNA synthetase

Query Match 90.3%; Score 28; DB 2; Length 573;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYPAR 6
 |:||||
 Db 31 FARYPAR 36

RESULT 15
 E64908
 peptidyl-dipeptidase Dcp (EC 3.4.15.5) - Escherichia coli (strain K-12)
 N/Alternate names: dipeptidyl carboxypeptidase II
 C/Species: Escherichia coli
 C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C/Accession: E64908; A49931; S14870
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A/Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: E64908
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A;Residues: 1-681 <BLAT>
 A;Cross-references: UNIPROT:P24171; UNIPARC:UPI00001680B4; GB:AE000251; GB:U00096; NID:G
 A;Experimental source: strain K-12, substrain MG1655
 R;Henrich, B.; Becker, S.; Schroeder, U.; Plapp, R.
 J. Bacteriol. 175, 7290-7300, 1993
 A/Title: dcp gene of Escherichia coli: cloning, sequencing, transcript mapping, and char
 A/Reference number: A49931; MUID:94042903; PMID:8226676
 A/Accession: A49931
 A;Status: preliminary
 A/Molecule type: DNA
 A;Residues: 1-138; 'LL', '141-681 <HEN>
 A;Cross-references: UNIPARC:UPI000016F0BD; GB:X57947; NID:G41243; PIDN:CAA41014.1; PID:G
 R;Becker, S.; Plapp, R.
 submitted to the EMBL Data Library, February 1991
 A/Reference number: S14870
 A/Accession: S14870
 A;Status: preliminary
 A/Molecule type: DNA
 A;Residues: 1-138; 'LL', '141-681 <BEC>
 A;Cross-references: UNIPARC:UPI000016F0BD; EMBL:X57947; NID:G41243; PIDN:CAA41014.1; PID
 C;Genetics:
 A;Gene: dcp
 C/Function:
 A;Note: zinc cofactor
 C;Superfamily: peptidyl-dipeptidase Dcp
 C;Keywords: metalloproteinase; peptidyl-dipeptide hydrolase; zinc

Query Match 90.3%; Score 28; DB 2; Length 681;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYPAR 6
 |:||||
 Db 515 FARYPAR 520

RESULT 16
 C90897
 dipeptidyl carboxypeptidase II [imported] - Escherichia coli (strain O157:H7, substrain
 C;Species: Escherichia coli
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C/Accession: C90897

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
 A/Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: C90897
 A;Status: preliminary
 A/Molecule type: DNA
 A;Residues: 1-681 <HAY>
 A;Cross-references: UNIPROT:Q8XB30; UNIPARC:UPI00000D0637; GB:BA000007; PIDN:BA835570.1;
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: EC92147
 C;Superfamily: peptidyl-dipeptidase Dcp

Query Match 90.3%; Score 28; DB 2; Length 681;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYPAR 6
 |:||||
 Db 515 FARYPAR 520

RESULT 17
 D85720
 dipeptidyl carboxypeptidase II [imported] - Escherichia coli (strain O157:H7, substrain I
 C;Species: Escherichia coli
 C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C/Accession: D85720
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
 Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A/Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: D85720
 A;Status: preliminary
 A/Molecule type: DNA
 A;Residues: 1-681 <STO>
 A;Cross-references: UNIPROT:Q8XB30; UNIPARC:UPI00000D0637; GB:AE005174; NID:G12515118; PJ
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: dcp
 C;Superfamily: peptidyl-dipeptidase Dcp

Query Match 90.3%; Score 28; DB 2; Length 681;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYPAR 6
 |:||||
 Db 515 FARYPAR 520

RESULT 18
 AC2211
 heme transport protein alx2242 [imported] - Nostoc sp. (strain PCC 7120)
 C/Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C/Accession: AC2211
 R;Kaneoki, T.; Nakamura, Y.; Wolk, C.P.; Kurtz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AC2211
 A;Status: preliminary
 A/Molecule type: DNA
 A;Residues: 1-877 <KUR>
 A;Cross-references: UNIPROT:Q8YS49; UNIPARC:UPI00000CE703; GB:BA000019; PIDN:BA874941.1;
 A;Experimental source: strain PCC 7120
 C;Genetics:

A:Gene: alx3242

Query Match 90.3%; Score 28; DB 2; Length 877;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
 |||||
 601 FSRYSR 606

Db 601 FSRYSR 606

RESULT 19

hypothetical protein PA3728 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: D83181
 R/Stover, C.K.; Pham, X.Q.; Ewlin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A/Reference number: A82950; WUID:20437337; PMID:10984043
 A/Accession: D83181
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1746 <STO>
 A/Cross-references: UNIPROT:Q9HXR4; UNIPARC:UPI00000C5AE2; GB:AE004791; GB:AE004091; NID
 A/Experimental source: strain PA01
 C/Genetics:

A:Gene: PA3728

Query Match 90.3%; Score 28; DB 2; Length 1746;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
 |||||
 1099 FSRVAR 1104

Db 1099 FSRVAR 1104

RESULT 20

hypothetical protein At2g37350 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: F84791
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Molnar, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talton, L.
 eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A/Reference number: A84420; WUID:20083487; PMID:10617197
 A/Accession: F84791
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-36 <STO>
 A/Cross-references: UNIPROT:Q9FYA7; UNIPROT:Q9FYB7; UNIPROT:Q8VYA5; UNIPARC:UPI000017A6F
 C/Genetics:

A:Gene: At2g37350

A:Map position: 2

Query Match 87.1%; Score 27; DB 2; Length 36;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRVAR 6
 |||||
 31 FSRYGR 36

Db 31 FSRYGR 36

RESULT 21

AI0982

hypothetical protein STY4163 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typh
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A/Note: this species has also been called *Salmonella typhi*
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AI0982
 R/Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Comeran, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moulé, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serova
 A/Reference number: AB0502; WUID:21534947; PMID:11677608
 A/Accession: AI0982
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-43 <PAR>
 A/Cross-references: UNIPARC:UPI000005A744; GB:AL513382; PIDN:CAD07989.1; PID:g16504975; C
 C/Genetics:

A:Gene: STY4163

Query Match 87.1%; Score 27; DB 2; Length 43;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
 |||||
 16 FSRVAR 21

Db 16 FSRVAR 21

RESULT 22

VC033 protein homolog (AF179595) [imported] - *Agrobacterium tumefaciens* (strain C58, Cere
 C:Species: *Agrobacterium tumefaciens*
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C/Accession: F97521
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Mollam, C.; Allinger, M.; Doughny, D.; Scott, C.; Lappas, C.; Marxeltz, B.;
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tume*
 A/Reference number: A97359; WUID:21608551; PMID:11743194
 A/Accession: F97521
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <KUR>
 A/Cross-references: UNIPROT:Q8UFR1; UNIPARC:UPI00000D1B08; GB:AE007869; PIDN:AAK87127.1;
 C/Genetics:

A:Gene: AGR_C_2462

A:Map position: circular chromosome

Query Match 87.1%; Score 27; DB 2; Length 108;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRVAR 6
 |||||
 18 FSRVAR 23

Db 18 FSRVAR 23

RESULT 23

conserved hypothetical protein Atu1336 [imported] - *Agrobacterium tumefaciens* (strain C58
 C:Species: *Agrobacterium tumefaciens*
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C/Accession: AH2740
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erge, G.; Gille, W.; Grant, C.; Gunthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan,
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A/Reference number: AB2577; WUID:21608550; PMID:11743193
 A/Accession: AH2740

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <KUR>
A:Cross-references: UNIPROT:Q8UFRI; UNIPARC:UPI00000D1B08; GB:AE008688; P1DN:AAI42342.1;
C:Genetics:
A:Gene: Atu1336
A:Map position: circular chromosome

Query Match 87.1%; Score 27; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
Db 18 FSRYPAR 23

RESULT 24

B84920
hypothetical protein At2g47840 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84920

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84920

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-208 <STO>
A:Cross-references: UNIPROT:O82251; UNIPARC:UPI00000A1EFL; GB:AE002093; NID:3738296; P1
C:Genetics:
A:Gene: At2g47840
A:Map position: 2

Query Match 87.1%; Score 27; DB 2; Length 208;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
Db 126 FSRYPAR 131

RESULT 25

B49547
nucleoside-diphosphate kinase (EC 2.7.4.6) precursor, mitochondrial - slime mold (Dictyo
C:Species: Dictyostelium discoideum
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Oct-2004
C:Accession: B49547
R;Troll, H.; Winkler, T.; Lascu, I.; Mueller, N.; Saurin, W.; Veron, M.; Muzel, R.
J. Biol. Chem. 268, 25469-25475, 1993
A:Title: Separate nuclear genes encode cytosolic and mitochondrial nucleoside diphosphat
A:Reference number: A49547; MUID:94064612; PMID:8244961
A:Accession: B49547

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <TKO>
A:Cross-references: UNIPARC:UPI0000175708; GB:L23068
C:Genetics:
A:Gene: gmk

A:Introns: 25/1; 80/3; 83/1; 173/2
C:Superfamily: nucleoside diphosphate kinase
C:Keywords: ATP binding; hexamer; mitochondrion; phosphonistidine; phosphoprotein; phosph
F;83-87/Region: ATP binding #status predicted
F;186/Active site: His (phosphonistidine intermediate) #status predicted

Query Match 87.1%; Score 27; DB 2; Length 220;
Best Local Similarity 83.3%; Pred. No. 75;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSRYPAR 6
Db 2 FSRYPAR 7

RESULT 26

JC4755
ribosomal protein L10.e, cytosolic - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: transcription factor
C:Species: Schizosaccharomyces pombe
C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4755; T39755
R;Masson, J.Y.; Vachais, J.; Ramotar, D.
Gene 170, 153-154, 1996

A:Title: The Schizosaccharomyces pombe spgM gene is a new member of the Qm transcription
A:Reference number: JC4755; MUID:96200877; PMID:8621081
A:Accession: JC4755

A:Molecule type: DNA
A:Residues: 1-232 <MAS>
A:Cross-references: UNIPROT:Q09127; UNIPARC:UPI0000168FD2; GB:U33214; NID:G1141785; P1DN:
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21878
A:Accession: T39755
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-69, '1', 71-220, 'A', <WMO>
A:Cross-references: UNIPARC:UPI0000133CD5; EMBL:AL035077; P1DN:CAA22664.1; GSPDB:GN00066;

A:Experimental source: strain 972h-; cosmid c18E5
C:Genetics:
A:Gene: spgM; SPDB:SPBC18E5.04
A:Map position: 1
C:Superfamily: ribosomal protein L10
C:Keywords: cytosol; protein biosynthesis; ribosome

Query Match 87.1%; Score 27; DB 2; Length 232;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
Db 173 FSRYPAR 178

RESULT 27

AE3245
hypothetical protein accE [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE3245
R;Wood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McLellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3245
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q8U604; UNIPARC:UPI00000027AF; GB:AE008690; P1DN:AAI46379.1;

A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: accE
A:Genome: plasmid
C:Superfamily: oligopeptide permease protein oppB

Query Match 87.1%; Score 27; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
| | | | |
Db 160 FERYAR 165

RESULT 28

T03434
probable transport protein accE - Agrobacterium tumefaciens plasmid pTIC58

C/Species: Agrobacterium tumefaciens
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C/Accession: T03434
R:Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwang, I.; Kim, H.; Farrand, S.K.

submitted to the EMBL Data Library, May 1998
A/Reference number: Z14943

A/Accession: T03434
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-286 <PIP>
A/Cross-references: UNIPROT:Q30544; UNIPARC:UPI0000089CE0; EMBL:AF010180; NID:93153171;

C/Genetics:
A/Gene: accE

A/Genome: plasmid pTIC58
C/Superfamily: oligopeptide permease protein oppB

Query Match 87.1%; Score 27; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
| | | | |
Db 160 FERYAR 165

RESULT 29

S35983

proline transport protein - Salmonella typhimurium

C/Species: Salmonella typhimurium
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S35983
R:Liao, M.K.; Maloy, S.

submitted to the EMBL Data Library, August 1993
A/Description: Identification of a cryptic proline transport system in Salmonella typhim

A/Reference number: S35983
A/Accession: S35983

A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-292 <LIA>
A/Cross-references: UNIPROT:P37460; UNIPARC:UPI000017AA90; EMBL:X74420

Query Match 87.1%; Score 27; DB 2; Length 292;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
| | | | |
Db 96 FSRYAR 101

RESULT 30

E87697

ddpP-4-dehydrohamose reductase [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C/Accession: E87697
R:Nierman, W.C.; Paulblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.

B.; Leub, M.T.; Deboy, R.T.; Dodson, R.O.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:1159647
A/Accession: E87697

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-293 <STO>
A/Cross-references: UNIPROT:Q9A2F0; UNIPARC:UPI00000C7B37; GB:AE005673; NID:913425365; P]

Query Match 87.1%; Score 27; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
| | | | |
Db 150 FSRYAR 155

RESULT 31

T45890

splicing factor-like protein - Arabidopsis thaliana

N/Alternate names: protein PAP12.200
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 05-Oct-2004
C/Accession: T45890

R:Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000

A/Reference number: Z23016
A/Accession: T45890

A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-302 <BLO>
A/Cross-references: UNIPROT:Q9FVB7; UNIPARC:UPI000017A395; EMBL:AL132966

A/Experimental source: cultivar Columbia; BAC clone F4P12
C/Genetics:
A/Map position: 3

A/Intons: 36/2; 41/3; 67/3; 99/3; 164/2; 198/2
A/Note: PAP12.200

Query Match 87.1%; Score 27; DB 2; Length 302;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
| | | | |
Db 31 FSRYAR 36

RESULT 32

JCS855

polyketide synthase (EC 2.-.-.-) chain 6 - Actinomyadura hibisca

C/Species: Actinomyadura hibisca
C/Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C/Accession: JCS855
R:Baird, T.; Hamano, Y.; Igarashi, Y.; Furumai, T.; Oki, T.

Biosci. Biotechnol. Biochem. 61, 1445-1453, 1997
A/Title: Cloning and nucleotide sequence of the putative polyketide synthase genes for p

A/Reference number: JCS850; MUID:97480928; PMID:9339544
A/Accession: JCS855
A/Molecule type: DNA

A/Residues: 1-341 <DAI>
A/Cross-references: UNIPROT:Q32456; UNIPARC:UPI000002F07D; DBJ:D87924; NID:92580441; PII

C/Comment: This enzyme catalyzes repeated condensation cycles of acyl-CoA, affecting the

C/Genetics:
A/Gene: pms6
C/Superfamily: O-methyltransferase

C/Keywords: transferase
Query Match 87.1%; Score 27; DB 2; Length 341;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
| | | | |

Db 171 FERRYAR 176

RESULT 33
C83575
fructose-1,6-bisphosphate aldolase PA0555 [imported] - Pseudomonas aeruginosa (strain PA
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83575
R/Stover, C.K.; Pham, X.Q.; Errin, A.L.; Mischuch, S.D.; Warriner, P.; Hickey, M.J.; Bz
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C83575
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-354 <STO>
A/Cross-references: UNIPROT:Q915Y1, UNIPARC:UPI0000125826; GB:AE004492; GB:AE004091; NID
C/Genetics:
A/Experimental source: strain PA01
A/Genes: fda; PA0555
C/Superfamily: fructose-bisphosphate aldolase II

Query Match 87.1%; Score 27; DB 2; Length 354;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FERRYAR 6
| | | | |
Db 341 FERRYAR 346

RESULT 34
E75080
3-phosphoglycerate kinase (pgk) PAB1679 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: E75080
R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A/Reference number: A75001
A/Accession: E75080
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-410 <KAM>
A/Cross-references: UNIPROT:Q9UZW0, UNIPARC:UPI0000034625; GB:AJ248286; GB:AL096836; NID
A/Experimental source: strain Orsay
C/Genetics:
A/Genes: PAB1679
C/Superfamily: phosphoglycerate kinase

Query Match 87.1%; Score 27; DB 2; Length 410;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FERRYAR 6
| | | | |
Db 91 FERRYAR 96

RESULT 35
D71065
probable phosphoglycerate kinase - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C/Accession: D71065
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: D71065
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-410 <KAM>
A/Cross-references: UNIPROT:Q58965; UNIPARC:UPI00001180B; GB:AP000005; NID:93236132; P
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Genes: PH1218
C/Superfamily: phosphoglycerate kinase

Query Match 87.1%; Score 27; DB 2; Length 410;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FERRYAR 6
| | | | |
Db 91 FERRYAR 96

RESULT 36
T15705
hypothetical protein C30B5.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15705
R/Du, Z.
submitted to the EMBL Data Library, July 1995
A/Description: sequence of C. elegans cosmid C30B5.
A/Reference number: S59417
A/Accession: T15705
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-411 <DUZ>
A/Cross-references: UNIPROT:Q18317, UNIPARC:UPI0000075091; EMBL:U23450; NID:97335552; P
A/Experimental source: strain Bristol N2
C/Genetics:
A/Genes: CESP:C30B5.3
A/Introns: 12/2; 91/1; 349/3

Query Match 87.1%; Score 27; DB 2; Length 411;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FERRYAR 6
| | | | |
Db 97 FERRYAR 102

RESULT 37
D87672
glutamate-cysteine ligase [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C/Accession: D87672
R/Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: D87672
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-453 <STO>
A/Cross-references: UNIPROT:Q9A2Z2, UNIPARC:UPI00000C7A81; GB:AE005673; NID:913425126; P
C/Genetics:
A/Genes: CC3414
C/Superfamily: glutamate--cysteine ligase

Query Match 87.1%; Score 27; DB 2; Length 453;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FSRYPAR 6
| | | | |
Db 250 FSRYPAR 255

RESULT 38

AH0551
proline-specific permease ProY [imported] - Salmonella enterica subsp. enterica serovar
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C/Accession: AH0551
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
Ch, T.; Connetton, P.; Crohin, A.; Davies, P.; Davies, R.W.; Dowd, L.; White, N.; Farrar,
S.; Moulie, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AH0551
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-456 <PAR>
A/Cross-references: UNIPARC:UPI000005A249; GB:AL513382; PIDN:CAD08856.1; PID:G16501669;
C/Genetics:
A/Gene: STRY0438
C/Superfamily: ecotropic retrovirus receptor protein

Query Match 87.1%; Score 27; DB 2; Length 456;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
| | | | |
Db 75 FSRYPAR 80

RESULT 39

B64769
proline transport protein - Escherichia coli (strain K-12)
N/Alternate names: proline permease; proline-specific permease
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: B64769
R/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: B64769
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-457 <BLAT>

A/Cross-references: UNIPROT:P77327; UNIPARC:UPI000013232F; GB:AE000146; GB:U00096; NID:G
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: ecotropic retrovirus receptor protein
C/Keywords: amino acid transport; transmembrane protein
F/3-59/Domain: transmembrane #status predicted <TM1>
F/96-112/Domain: transmembrane #status predicted <TM2>
F/125-141/Domain: transmembrane #status predicted <TM3>
F/157-173/Domain: transmembrane #status predicted <TM4>
F/241-257/Domain: transmembrane #status predicted <TM5>
F/279-295/Domain: transmembrane #status predicted <TM6>
F/330-346/Domain: transmembrane #status predicted <TM7>
F/357-373/Domain: transmembrane #status predicted <TM8>
F/403-419/Domain: transmembrane #status predicted <TM9>
F/429-445/Domain: transmembrane #status predicted <TM10>

Query Match 87.1%; Score 27; DB 2; Length 457;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
| | | | |
Db 75 FSRYPAR 80

RESULT 40

D90685
proline permease transport protein Ecs0452 [imported] - Escherichia coli (strain O157:H7,
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: D90685
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: D90685
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-457 <HAY>
A/Cross-references: UNIPROT:P77327; UNIPARC:UPI000013232F; GB:BA000007; PIDN:BA833875.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: Ecs0452
C/Superfamily: ecotropic retrovirus receptor protein

Query Match 87.1%; Score 27; DB 2; Length 457;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
| | | | |
Db 75 FSRYPAR 80

RESULT 41

H85535
proline permease transport protein [imported] - Escherichia coli (strain O157:H7, substra
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: H85535
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamouotis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: H85535
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-457 <STO>
A/Cross-references: UNIPROT:P77327; UNIPARC:UPI000013232F; GB:AE005174; NID:G12513248; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: proY
C/Superfamily: ecotropic retrovirus receptor protein

Query Match 87.1%; Score 27; DB 2; Length 457;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
| | | | |
Db 75 FSRYPAR 80

RESULT 42

A10388
probable proline-specific permease [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: A10388
R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AI0388
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-463 <KUR>
A/Cross-references: UNIPROT:Q8ZC25; UNIPARC:UPI00000CD9E2; GB:AL590842; PIDN:CAC92436.1;
C/Genetics:
A/Gene: *proX*
C/Superfamily: ecotropic retrovirus receptor protein

Query Match 87.1%; Score 27; DB 2; Length 463;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|
|
|
|
|
Db 77 FSRYAQ 82

RESULT 43
C42603
phospho-beta-glucosidase *ArbB* - *Erwinia chrysanthemi*
C/Species: *Erwinia chrysanthemi*
C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C/Accession: C42603
R/El Hassouni, M.; Henrissat, B.; Chipaux, M.; Barrae, F.
J. Bacteriol. 174, 765-777, 1992
A>Title: Nucleotide sequences of the *arb* genes, which control beta-glucoside utilization
in a family including enzymes from eubacteria, archaeobacteria, and humans.
A/Reference number: A42603; MUID:92121114; PMID:1732212
A/Accession: C42603
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-465 <ELI>
A/Cross-references: UNIPROT:P26206; UNIPARC:UPI0000175B1C
A/Note: sequence inconsistent with the nucleotide translation
C/Superfamily: *Agrobacterium* beta-glucosidase

Query Match 87.1%; Score 27; DB 2; Length 465;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
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|
|
|
|
Db 150 FERYAR 155

RESULT 44
C87351
aldehyde dehydrogenase [imported] - *Caulobacter crescentus*
C/Species: *Caulobacter crescentus*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: C87351
R/Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.O.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of *Caulobacter crescentus*.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: C87351
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-478 <STO>
A/Cross-references: UNIPROT:Q9A9Y9; UNIPARC:UPI00000C71A2; GB:AE005673; NID:gt13422073; F
C/Genetics:
A/Gene: CC0822
C/Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 87.1%; Score 27; DB 2; Length 478;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|
|
|
|
|
Db 423 FRYAR 428

RESULT 45
B86565
oligopeptide permease [imported] - *Chlamydia pneumoniae* (strain J138)
C/Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86565
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of *Chlamydia pneumoniae* J138.
A/Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: B86565
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-579 <STO>
A/Cross-references: UNIPROT:Q9Z7V7; UNIPARC:UPI0000043CB3; GB:BA000008; NID:98978969; PII
A/Experimental source: strain J138
C/Genetics:
A/Gene: *oppC_2*

Query Match 87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|
|
|
|
|
Db 455 FSRYVR 460

RESULT 46
C72059
peptide ABC transporter, permease protein, probable CP0151 [imported] - *Chlamydia pne*
C/Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: C72059; B81608
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.
A/Reference number: A72000; MUID:99206606; PMID:10192388
A/Accession: C72059
A/Molecule type: DNA
A/Residues: 1-579 <ARN>
A/Cross-references: UNIPROT:Q9Z7V7; UNIPARC:UPI0000043CB3; GB:AE001644; GB:AE001363; NID:
A/Experimental source: strain CMO129
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, F
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of *Chlamydia trachomatis* MOPn and *Chlamydia pneumoniae* AR39.
A/Reference number: A81500; MUID:20150285; PMID:10684935
A/Accession: B81608
A/Molecule type: DNA
A/Residues: 1-579 <REA>
A/Cross-references: UNIPARC:UPI0000043CB3; GB:AE002176; GB:AE002161; NID:97189080; PIDN:
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: *oppC_2*; CP0151

Query Match 87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|
|
|
|
|
Db 455 FSRYVR 460

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RESULT 47
S16561
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Rhizobium meli
N:Alternate names: glutamine-fructose-6-phosphate aminotransferase
C:Species: Rhizobium melioli
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S16561
R:Raey, N.; Endre, G.; Petrovic, G.; Banfalvi, Z.; Kondorosi, A.
Mol. Gen. Genet. 228, 113-124, 1991
A>Title: Six nodulation genes of nod box locus 4 in Rhizobium melioli are involved in n
A:Reference number: S16561; MUID:91360053; PMID:1909418
A:Accession: S16561
A:Molecule type: DNA
A:Residues: 1-605 <RAE>
A:Cross-references: UNIPROT:P25195; UNIPARC:UPI000016FEF8; EMBL:X58632; NID:g46331; PIDN
C:Function:
A>Description: catalyzes the formation of D-glucosamine-6-phosphate from the amido group
A:Pathway: glucosamine biosynthesis
A>Note: glucosamine-6-phosphate is used in the biosynthesis of amino sugars of asparagin
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C:Keywords: aminotransferase; isomerase
F:2-605/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predi
F:2/Active site: Cys #status predicted

Query Match      87.1%; Score 27; DB 2; Length 605;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 311 FERYAR 316

RESULT 48
S01040
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Rhizobium legu
N:Alternate names: nodulation protein nodM
C:Species: Rhizobium leguminosarum bv. viciae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S01040
R:Surin, B.P.; Downie, J.A.
Mol. Microbiol. 2, 173-183, 1988
A>Title: Characterization of the Rhizobium leguminosarum genes nodLMN involved in effici
A:Reference number: S01039; MUID:88246045; PMID:3132583
A:Accession: S01040
A:Molecule type: DNA
A:Residues: 1-608 <SUR>
A:Cross-references: UNIPROT:P08633; UNIPARC:UPI000016FEF7B; EMBL:Y00548; NID:g46212; PIDN
C:Genetics:
A:Gene: nodM
A:Genome: plasmid pRL1J1
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C:Keywords: aminotransferase; isomerase; nodulation
F:2-608/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predi
F:2/Active site: Cys #status predicted

Query Match      87.1%; Score 27; DB 1; Length 608;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 312 FERYAR 317

RESULT 49
C97575
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Agrobacterium
N:Alternate names: glucosamine-fructose-6-P aminotransferase (mismomer)
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97575

```

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R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,
A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C97575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <KUR>
A:Cross-references: UNIPROT:Q8UEH1; UNIPARC:UPI00001643A5; GB:AE007869; PIDN:AAK87556.1;
C:Genetics:
A:Gene: AGR_C3284
A:Map position: circular chromosome
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C:Keywords: aminotransferase; isomerase

Query Match      87.1%; Score 27; DB 2; Length 608;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 312 FERYAR 317

RESULT 50
AC2796
hypothetical protein glms [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC2796
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gallet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; Mccllell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, K
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC2796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <KUR>
A:Cross-references: UNIPROT:Q8UEH1; UNIPARC:UPI00001643A5; GB:AE008686; PIDN:AAU42785.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: glms
A:Map position: circular chromosome
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)

Query Match      87.1%; Score 27; DB 2; Length 608;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 312 FERYAR 317

Search completed: August 29, 2006, 06:14:22
Job time : 13 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 05:47:27 ; Search time 48 Seconds
(without alignments)
115.627 Million cell updates/sec

Title: US-10-541-343-2

Perfect score: 31

Sequence: 1 PSRYAR 6

Scoring table: BLOSUM62
Gapop.10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	100.0	324	2	Q2SEI3_GGAMM	Q2SEI3 habella che
2	31	100.0	338	2	Q7Q9K9_AMOGA	Q7Q9K9 anopheles g
3	31	100.0	356	1	PAAB_ECOLI	P76081 escherichia
4	31	100.0	357	1	MURG_CHLUP	P92702 chlamydia p
5	31	100.0	412	2	O5SMX2_ORYSA	O5SMX2 oryza sativ
6	31	100.0	427	2	O98L45_RHIO	O98L45 rhizobium l
7	31	100.0	432	2	O5JIL5_ALCPA	O5JIL5 alcaligenes
8	31	100.0	447	2	Q62CX5_BURMA	Q62CX5 burkholderi
9	31	100.0	460	2	Q45AY3_9BURK	Q45AY3 burkholderi
10	31	100.0	460	2	Q41T22_9BURK	Q41T22 burkholderi
11	31	100.0	460	2	Q39SV1_BURR3	Q39SV1 burkholderi
12	31	100.0	461	2	Q2T4Z4_BURPH	Q2T4Z4 burkholderi
13	31	100.0	461	2	Q3JFR3_BURP1	Q3JFR3 burkholderi
14	31	100.0	461	2	Q63M15_BURPS	Q63M15 burkholderi
15	31	100.0	463	2	Q346I8_BACSV	Q346I8 bacillus su
16	31	100.0	468	2	Q2STX5_BURTH	Q2STX5 burkholderi
17	31	100.0	468	2	Q3JY99_BURP1	Q3JY99 burkholderi
18	31	100.0	468	2	Q62G62_BURMA	Q62G62 burkholderi
19	31	100.0	468	2	Q63PW6_BURPS	Q63PW6 burkholderi
20	31	100.0	474	1	ASCB_ECOLI	P24240 escherichia
21	31	100.0	474	2	Q31X80_SHIDS	Q31X80 shigella bo
22	31	100.0	474	2	Q32CL4_SHIDS	Q32CL4 shigella dy
23	31	100.0	474	2	Q3YEB8_SHIDS	Q3YEB8 shigella so
24	31	100.0	474	2	Q2MAB3_ECOLI	Q2MAB3 escherichia
25	31	100.0	474	2	Q8X941_RCO57	Q8X941 escherichia
26	31	100.0	494	2	Q3KAM6_PSEBP	Q3KAM6 pseudomonas
27	31	100.0	496	2	Q2X8L3_PSEPU	Q2X8L3 pseudomonas
28	31	100.0	496	2	Q88FQ2_PSEBP	Q88FQ2 pseudomonas
29	31	100.0	496	2	Q91674_PSEBP	Q91674 pseudomonas
30	31	100.0	526	2	Q3BYW8_XANCS	Q3BYW8 xanthomonas
31	31	100.0	526	2	Q8PQL8_XANNC	Q8PQL8 xanthomonas

32	31	100.0	560	2	Q7SA29_NEUCR	Q7SA29 neurospora
33	31	100.0	635	2	Q21882_RHOPA	Q21882 rhodospseudo
34	31	100.0	663	2	Q374J7_RHOPA	Q374J7 rhodospseudo
35	31	100.0	809	2	Q4SCU9_TETNG	Q4SCU9 tetracton n
36	31	100.0	1427	2	Q4P6R1_USTMA	Q4P6R1 ustilago ma
37	31	100.0	1429	2	Q57UM9_9TRYP	Q57UM9 trypanosoma
38	31	100.0	1649	2	Q8WMB3_9TRYP	Q8WMB3 trypanosoma
39	28	90.3	37	2	Q49100_MYCCA	Q49100 mycoplasma
40	28	90.3	102	2	Q56EC7_9CAUD	Q56EC7 aeromonas p
41	28	90.3	110	2	Q5UJN8_BRARE	Q5UJN8 brachydanio
42	28	90.3	126	2	Q5ZJM2_CHICK	Q5ZJM2 gallus gall
43	28	90.3	133	2	Q3YQB8_BURP1	Q3YQB8 burkholderi
44	28	90.3	170	2	Q52KS6_XENIA	Q52KS6 xenopus lae
45	28	90.3	170	2	Q6DRM0_BRARE	Q6DRM0 brachydanio
46	28	90.3	171	2	Q5AAP5_CANAL	Q5AAP5 candida alb
47	28	90.3	174	1	WRB_HUMAN	WRB_HUMAN
48	28	90.3	174	1	WRB_MOUSE	WRB_MOUSE
49	28	90.3	174	1	WRB_PONPY	WRB_PONPY
50	28	90.3	174	1	WRB_RAT	WRB_RAT
51	28	90.3	174	2	Q3S2Z6_BOVIN	Q3S2Z6 bovis taurus
52	28	90.3	174	2	Q7MXS1_RALEU	Q7MXS1 ralestonia e
53	28	90.3	174	2	Q3TAS5_MOUSE	Q3TAS5 mus musculu
54	28	90.3	174	2	Q52MA2_XENIA	Q52MA2 xenopus lae
55	28	90.3	220	2	Q3EBU3_ARYTH	Q3EBU3 arabidopsis
56	28	90.3	227	2	Q3CFN6_THRET	Q3CFN6 thermoanaer
57	28	90.3	231	2	Q7XZAI_GRIJA	Q7XZAI griffithsia
58	28	90.3	239	2	Q239S9_SORYB	Q239S9 glycine max
59	28	90.3	243	2	Q7XQ03_ORYSA	Q7XQ03 oryza sativ
60	28	90.3	243	2	Q9PLN9_ARYTH	Q9PLN9 arabidopsis
61	28	90.3	256	2	Q3USC3_BURP1	Q3USC3 burkholderi
62	28	90.3	256	2	Q62KE8_BURMA	Q62KE8 burkholderi
63	28	90.3	256	2	Q63U80_BURPS	Q63U80 burkholderi
64	28	90.3	278	2	Q3N1J7_9DELT	Q3N1J7 syntrophoba
65	28	90.3	283	2	Q22323_CABEL	Q22323 caenorhabdi
66	28	90.3	292	2	Q2SW01_BURTH	Q2SW01 burkholderi
67	28	90.3	301	2	Q6UFY8_HORYU	Q6UFY8 hordeum vul
68	28	90.3	306	2	Q4MSJ1_BACCE	Q4MSJ1 bacillus ce
69	28	90.3	306	2	Q63B07_BACCE	Q63B07 bacillus ce
70	28	90.3	306	2	Q6HLI2_BACHK	Q6HLI2 bacillus th
71	28	90.3	306	2	Q81TA2_BACAN	Q81TA2 bacillus an
72	28	90.3	306	2	Q73BD6_BACCI	Q73BD6 bacillus ce
73	28	90.3	322	1	NODZ_RHISN	P55355 rhizobium s
74	28	90.3	322	2	O85712_RHIFR	O85712 rhizobium f
75	28	90.3	323	2	Q72VH4_LEPIC	Q72VH4 leprospira
76	28	90.3	323	2	Q8E921_LEPIN	Q8E921 leprospira
77	28	90.3	324	2	Q9AQ17_BRASW	Q9AQ17 bradyrhizob
78	28	90.3	327	2	Q4ASB0_MYC55	Q4ASB0 mycoplasma
79	28	90.3	328	2	Q49HK6_9BACT	Q49HK6 uncultured
80	28	90.3	328	2	Q8KUG7_RHRET	Q8KUG7 rhizobium e
81	28	90.3	329	2	Q8KJ52_RHIL0	Q8KJ52 rhizobium l
82	28	90.3	329	2	Q98AU6_RHIL0	Q98AU6 rhizobium l
83	28	90.3	339	2	Q5X1J2_RAT	Q5X1J2 rattus norv
84	28	90.3	360	2	Q3G6O6_9DELT	Q3G6O6 pseudocater
85	28	90.3	364	2	Q71AA4_9NUCL	Q71AA4 mamestra co
86	28	90.3	364	2	Q8OLC6_9NUCL	Q8OLC6 mamestra co
87	28	90.3	370	1	NODZ_BRATA	Q45271 bradyrhizob
88	28	90.3	372	2	Q70S28_CROSA	Q70S28 crocus sativ
89	28	90.3	377	2	Q6FUJ8_CANGA	Q6FUJ8 candida gla
90	28	90.3	382	2	Q6FUL7_CANGA	Q6FUL7 candida gla
91	28	90.3	397	2	Q92072_RHIME	Q92072 rhizobium m
92	28	90.3	399	2	Q4CH65_CLOTHM	Q4CH65 clostridium
93	28	90.3	409	2	Q8YJDI_BRUME	Q8YJDI bruceella me
94	28	90.3	420	2	Q3CKC0_THRET	Q3CKC0 thermoanaer
95	28	90.3	437	2	Q92X34_RHIME	Q92X34 rhizobium m
96	28	90.3	445	1	FDPF_YAZOI	Q9Y153 yarrowia li
97	28	90.3	448	2	Q4IY65_ACOVT	Q4IY65 aerobacter
98	28	90.3	468	2	Q3SIH2_THIDA	Q3SIH2 thiodacidu
99	28	90.3	472	2	Q3JAX0_NITOC	Q3JAX0 nitrosococ
100	28	90.3	473	2	Q6ACI1_LEIIX	Q6ACI1 leifeonia x
101	28	90.3	475	2	Q92Y97_RHIME	Q92Y97 rhizobium m
102	28	90.3	476	2	Q61V14_PECOC	Q61V14 peccobacter
103	28	90.3	476	2	Q6D574_ERWCT	Q6D574 erwina car
104	28	90.3	479	2	Q89DW4_BRATA	Q89DW4 bradyrhizob

105	28	90.3	486	2	Q4AP9_9BURK	Q4aqp9	polaronomas	178	27	87.1	222	2	Q6ANCI_BACFR	Q6anc1	bacterioides
106	28	90.3	487	2	Q6BMH4_DEBHA	Q6bmh4	debaromyce	179	27	87.1	224	2	Q8PSA6_METWA	Q8psa6	methanosarc
107	28	90.3	487	2	Q8FYG8_BRUBA	Q8fyg8	brucella su	180	27	87.1	228	2	Q3SLM8_THIDA	Q3slm8	thiobacilli
108	28	90.3	495	2	Q4KDW7_PSEFS	Q4kdw7	pseudomonas	181	27	87.1	240	2	Q5YB90_9SPNN	Q5yb90	sphingomon
109	28	90.3	496	2	Q3H3P9_9ACTO	Q3h3p9	nocardioide	182	27	87.1	243	2	Q7PUZ1_ANOGA	Q7puz1	anopheles g
110	28	90.3	502	1	AMPA_DESPS	Q6ajz2	desulfocale	183	27	87.1	243	2	Q7OKY3_ANOGA	Q7oky3	anopheles g
111	28	90.3	538	2	Q6ESG6_ORYSA	Q6esg6	oryza sativ	184	27	87.1	244	2	Q6OTU2_CABER	Q6otu2	caenorhabdl
112	28	90.3	548	2	Q4WCP9_ASPFU	Q4wcp9	aspergillus	185	27	87.1	250	2	Q6ZZK6_ACTT1	Q6zzk6	actinophane
113	28	90.3	548	2	Q6MEX0_PARUW	Q6mex0	parachlamyd	186	27	87.1	257	2	Q2NV49_SODOL	Q2nv49	sodalis glo
114	28	90.3	571	1	SYM_SULAC	Q4j8m3	parachlamyd	187	27	87.1	270	2	Q4NF90_9MICC	Q4nf90	arctobacte
115	28	90.3	571	1	SYM_SULSO	Q571c1	escherichia	188	27	87.1	272	2	Q5V3V7_HALMA	Q5v3v7	halocaula
116	28	90.3	573	1	SYM_SULSO	Q5uww2	sulfolobus	189	27	87.1	276	2	Q6MPB5_BDBEA	Q6mpb5	bellowvibri
117	28	90.3	576	2	Q9FD23_PPSED	Q9fd23	pseudomonas	190	27	87.1	284	2	Q9FYB7_ARATH	Q9fyb7	arabidopsis
118	28	90.3	582	2	Q8H399_ORYSA	Q8h399	oryza sativ	191	27	87.1	286	2	Q30544_9RH12	Q30544	agrobacteri
119	28	90.3	605	2	Q2UUI2_ASPOR	Q2uui2	aspergillus	192	27	87.1	286	2	Q9REd6_9RH12	Q9red6	agrobacteri
120	28	90.3	658	2	Q2M4B7_MAGSA	Q2m4b7	magnetospir	193	27	87.1	286	2	Q8U6O4_AGRF5	Q8u6o4	arabidopsi
121	28	90.3	680	1	DCP_RCOLI	P24171	magnetospir	194	27	87.1	288	2	Q303R5_STREU	Q303r5	streptococ
122	28	90.3	680	2	Q4O3H9_LEIMA	Q4g3h9	leishmania	195	27	87.1	290	2	Q67Y02_ARATH	Q67y02	arabidopsi
123	28	90.3	681	2	Q320N6_SHIBS	Q320n6	shigella bo	196	27	87.1	290	2	Q8VYAS_ARATH	Q8vyas	arabidopsi
124	28	90.3	681	2	Q32G39_SHIDS	Q32g39	shigella dy	197	27	87.1	290	2	Q9FYA7_ARATH	Q9fya7	arabidopsi
125	28	90.3	681	2	Q32IS4_SHISS	Q32is4	shigella so	198	27	87.1	293	2	Q44EV3_CHRSL	Q44ev3	chromalob
126	28	90.3	681	2	Q7UCH1_SHIFL	Q7uch1	shigella fl	199	27	87.1	293	2	Q9A2F0_CAUCR	Q9a2f0	caulobacter
127	28	90.3	681	2	Q83L24_SHIFL	Q83l24	shigella fl	200	27	87.1	299	2	Q31K57_SYNP7	Q31k57	synecococ
128	28	90.3	681	2	Q8XB30_TCOE5	Q8xb30	escherichia	201	27	87.1	303	2	Q5JSP3_HUMAN	Q5jsp3	homo sapien
129	28	90.3	686	2	Q4SOZ9_TERTNG	Q4sgz9	tetracodon n	202	27	87.1	312	2	Q5SCB1_ORTTA	Q5scb1	ostreococu
130	28	90.3	703	2	Q8FHD3_ECOLI	Q8fhd3	escherichia	203	27	87.1	315	2	Q6Z9P6_ORYSA	Q6z9p6	oryza sativ
131	28	90.3	758	2	Q4BD58_BURVI	Q4bd58	burkholderi	204	27	87.1	315	2	Q5NIQ2_SYNP6	Q5niq2	synecococ
132	28	90.3	766	2	Q3IN21_SYNP7	Q3in21	synecococ	205	27	87.1	338	2	Q751R8_ORYSA	Q751r8	oryza sativ
133	28	90.3	766	2	Q5M2Z7_SYNP6	Q5m2z7	synecococ	206	27	87.1	338	2	Q40XX5_KINRA	Q40xx5	kinococcus
134	28	90.3	822	2	Q5LIG5_BACFN	Q5lig5	bacteroides	207	27	87.1	341	2	Q324S6_9ACTO	Q324s6	actinomadu
135	28	90.3	877	2	Q8Y849_ANASP	Q8y849	anaeana sp	208	27	87.1	341	2	Q62L28_BURMA	Q62l28	burkholderi
136	28	90.3	878	2	Q38BP9_9TRYP	Q38bp9	trypanosoma	209	27	87.1	341	2	Q63RY2_BURPS	Q63ry2	burkholderi
137	28	90.3	898	2	Q6MT97_MYCCA	Q6mt97	mycoplasma	210	27	87.1	346	2	Q2XC25_PSEBP	Q2xc25	pseudomonas
138	28	90.3	899	2	Q2SSJ3_MYCCA	Q2ssj3	mycoplasma	211	27	87.1	346	2	Q88N98_PSEBP	Q88n98	pseudomonas
139	28	90.3	927	2	Q4WML1_ASPFU	Q4wml1	aspergillus	212	27	87.1	349	2	Q4BR35_BURVI	Q4br35	burkholderi
140	28	90.3	936	2	Q9DMD4_RCMWU	Q9dmd4	rat cytoleg	213	27	87.1	354	1	ALF_PSEBA	Alf	pseba
141	28	90.3	970	2	Q91TM6_TUHYV	Q91tme	tupaiid her	214	27	87.1	354	2	Q48CH9_PSE14	Q48ch9	pseudomonas
142	28	90.3	993	2	Q4WYV7_ASPFU	Q4wyv7	aspergillus	215	27	87.1	354	2	Q4ZM08_PSEU2	Q4zm08	pseudomonas
143	28	90.3	1005	2	Q7NNY2_GLOVI	Q7nnv2	gloeobacter	216	27	87.1	354	2	Q2SLS8_9GAMU	Q2sls8	habbilla che
144	28	90.3	1064	2	Q74FA0_GEOSL	Q74fa0	grobacter s	217	27	87.1	354	2	Q88AK0_PSESM	Q88ak0	pseudomonas
145	28	90.3	1069	2	Q47ZS2_GOLP3	Q47zsz	colwellia p	218	27	87.1	355	2	Q4LEY6_9ENTR	Q4ley6	klebsiella
146	28	90.3	1205	2	Q5F9S0_NIEIG	Q5f9s0	nissieria g	219	27	87.1	357	2	Q3PAH8_9GAMM	Q3pah8	shewanella
147	28	90.3	1242	2	Q4SS72_TERTNG	Q4ss72	tetracodon n	220	27	87.1	360	2	Q92QY9_RHIME	Q92qy9	rhizobium m
148	28	90.3	1746	2	Q9HXK4_PSEAE	Q9hxt4	pseudomonas	221	27	87.1	365	2	Q4NGZ5_9MITC	Q4ngz5	arctobacte
149	28	90.3	2168	2	Q90Z47_BRARE	Q90z47	brachydanio	222	27	87.1	366	2	Q5BLUF_BRARE	Q5bluf5	brachydanio
150	28	90.3	2196	2	Q5TZF1_BRARE	Q5tze1	brachydanio	223	27	87.1	368	2	Q57U70_9TRYP	Q57u70	trypanosoma
151	28	90.3	2289	2	Q2LYX1_DROPS	Q2lyx1	drosochilla	224	27	87.1	374	2	Q6A4W3_9ANNE	Q6a4w3	namelycasti
152	28	90.3	2401	2	Q7RFS2_PLAYO	Q7rfes	plasmodium	225	27	87.1	374	2	Q65A40_ORYSA	Q65a40	oryza sativ
153	27	87.1	443	2	Q8Z2A2_SALT1	Q8z2a2	salmonella	226	27	87.1	378	2	Q3WZ29_9ACTO	Q3wz29	frankia sp.
154	27	87.1	102	2	Q6U965_9CAUD	Q6u965	aeromonas p	227	27	87.1	383	2	Q3WK33_ANAVT	Q3wk33	anaeana va
155	27	87.1	103	2	Q2LYE1_9DELT	Q2lye1	synetrophus	228	27	87.1	384	2	Q560P4_CRYNE	Q560p4	cryptococcu
156	27	87.1	107	2	Q5LMH4_SILPO	Q5lmh4	silicibacte	229	27	87.1	384	2	Q5KPF6_CRYNE	Q5kpf6	cryptococcu
157	27	87.1	108	2	Q8UFM1_AGRF5	Q8ufm1	agrobacteri	230	27	87.1	389	2	Q2IMC0_9DELT	Q2imc0	anaeromxob
158	27	87.1	126	2	Q424A3_DESHA	Q424a3	desulfifloba	231	27	87.1	390	2	Q6A4W2_9ANNE	Q6a4w2	namelycasti
159	27	87.1	128	2	Q43ZB5_SOLUS	Q43zb5	solibacter	232	27	87.1	391	2	Q3W9V8_9ACTO	Q3w9v8	frankia sp.
160	27	87.1	134	2	Q4VXS1_VIGMU	Q4vxs1	vigna mungo	233	27	87.1	391	2	Q742T7_MYCPA	Q742t7	mycobacteri
161	27	87.1	137	2	Q2QZN6_ORYSA	Q2qzn6	oryza sativ	234	27	87.1	396	2	Q59W18_CANAL	Q59w18	canida alb
162	27	87.1	145	2	Q8MWE0_BENMO	Q8mwe0	penaeus mon	235	27	87.1	400	2	Q4HRB7_CAMUP	Q4hrb7	campylobact
163	27	87.1	153	2	Q6W196_9ACTO	Q6w196	frankia sp.	236	27	87.1	401	2	Q4HH16_CAMCO	Q4hh16	campylobact
164	27	87.1	171	2	Q6DU58_THELAN	Q6du58	helianthus	237	27	87.1	403	2	Q74XK2_MYCPA	Q74xk2	mycobacteri
165	27	87.1	175	2	Q8ZVAS_NITEU	Q8zvas	nitrosomona	238	27	87.1	410	1	PGK_PYFAB	PGK	pyrococcus
166	27	87.1	183	2	Q813H6_PLAF7	Q813h6	plasmodium	239	27	87.1	410	2	PGK_PYRHO	PGK	pyrococcus
167	27	87.1	186	2	Q2IXV0_RHOAP	Q2ixv0	rhodopseudo	240	27	87.1	412	1	Q9XSC4_RABIT	Q9xsc4	oryctolagus
168	27	87.1	208	2	Q822S1_ARATH	Q822s1	arabidopsi	241	27	87.1	422	1	CPB2_CABEL	CPB2	caenorhabdl
169	27	87.1	208	2	Q94A61_ARATH	Q94a61	arabidopsi	242	27	87.1	423	2	Q3GI97_9DELT	Q3gi97	pelobacter
170	27	87.1	209	2	Q8LBB6_ARATH	Q8lbb6	arabidopsi	243	27	87.1	425	2	Q5JSP2_HUMAN	Q5jsp2	homo sapien
171	27	87.1	219	2	Q9FM67_ARATH	Q9fm67	arabidopsi	244	27	87.1	441	2	Q4SBP0_TERTNG	Q4sbp0	tetracodon n
172	27	87.1	219	2	Q2VZX2_MAGSA	Q2vzx2	magnetospir	245	27	87.1	442	2	Q84170_9POXV	Q84170	orf virus
173	27	87.1	220	1	NDKM_DICDI	P34093	dictyosceli	246	27	87.1	448	2	Q7VXU5_BORPE	Q7vxu5	bordeletia
174	27	87.1	220	1	Q54WJ3_DICDI	Q54wj3	dictyosceli	247	27	87.1	448	2	Q7W1W7_BORBR	Q7w1w7	bordeletia
175	27	87.1	221	1	RLIOA_SCHPO	Q09127	schistosach	248	27	87.1	451	2	Q41JJ2_METBU	Q41jj2	methanococ
176	27	87.1	221	1	RLIOB_SCHPO	Q9p766	schistosach	249	27	87.1	452	2	Q6TWY1_9POXV	Q6twy1	orf virus
177	27	87.1	222	2	Q5L844_BACFN	Q5l844	bacterioides	250	27	87.1	453	2	Q9A2Z2_CAUCR	Q9a2z2	caulobacter

251	27	87.1	453	2	06TM91_9POXV	06TM91_orf_virus.	324	27	87.1	581	2	Q2IEU8_9DELT	Q2IEU8_aeaeomyxob
252	27	87.1	455	2	05XKG4_GEOKA	05XKG4_geobacillus	325	27	87.1	583	2	Q3B612_PELLD	Q3B612_peloidicyon
253	27	87.1	456	1	PROT_SALTU	P37460_salmoneila	326	27	87.1	589	2	081013_CAEBL	081013_caenorthabdi
254	27	87.1	456	2	05PPT1_SALPA	05PPT1_salmoneila	327	27	87.1	592	1	S23A2_RAT	09UW8_rattus_nov
255	27	87.1	456	2	08Z8Y3_SALTU	P04853_salmoneila	328	27	87.1	594	1	CPB2_CAEDA	06E3F0_caenorthabdi
256	27	87.1	457	1	PROX_ECOS7	P04854_escherichia	329	27	87.1	601	2	Q7NTV6_CHRVO	Q7NTV6_chromobacte
257	27	87.1	457	1	PROX_ECOL6	P04855_escherichia	330	27	87.1	604	1	NODM2_RHIME	P25195_rhizobium_m
258	27	87.1	457	1	PROX_ECOL1	P04856_escherichia	331	27	87.1	606	1	GLMS_RHITO	0981X5_r_glucosam
259	27	87.1	457	1	PROX_ECOL1	P04857_escherichia	332	27	87.1	607	1	GLMS_AGRIS	08Aeh1_glucoam
260	27	87.1	457	2	Q3Z507_SHISS	Q3Z507_shigella_so	333	27	87.1	607	1	GLMS_RHIME	092P84_r_glucosam
261	27	87.1	457	2	Q2NNA5_9SPHN	Q2NNA5_erythrobact	334	27	87.1	607	1	NODM1_RHIME	0922K3_rhizobium_m
262	27	87.1	457	2	Q2MC24_ECOLI	Q2MC24_escherichia	335	27	87.1	607	1	NODM1_RHITV	P08633_rhizobium_1
263	27	87.1	457	2	Q3Z508_SHISS	Q3Z508_shigella_bo	336	27	87.1	607	2	Q2UPA8_ASPOR	Q2UPA8_aspergillus
264	27	87.1	457	2	Q3Z1F4_SHIDS	Q3Z1F4_shigella_dy	337	27	87.1	607	2	08KJH6_RHITO	08KJH6_rhizobium_1
265	27	87.1	457	2	083SG9_SHIFL	083SG9_shigella_fl	338	27	87.1	607	2	0988E3_RHITO	0988E3_rhizobium_1
266	27	87.1	458	2	06D860_ERWCT	06D860_erynia_car	339	27	87.1	607	2	0989K4_RHITO	0989K4_rhizobium_1
267	27	87.1	463	2	08D167_YERPE	08D167_yersinia_pe	340	27	87.1	608	2	Q2X8G1_RHLET	Q2X8G1_rhizobium_e
268	27	87.1	463	2	066DX2_YERPS	066DX2_yersinia_ps	341	27	87.1	610	2	Q7RD29_9VTRU	Q7RD29_oyster_mush
269	27	87.1	463	2	Q7NYY4_CHRVO	Q7NYY4_chromobacte	342	27	87.1	615	2	Q706Q0_PSEPU	Q706Q0_pseudomonas
270	27	87.1	463	2	08ZC25_YERPE	08ZC25_yersinia_pe	343	27	87.1	619	2	Q7JM92_CAEBL	Q7JM92_caenorthabdi
271	27	87.1	464	1	CASB_KTEOX	Q48409_klebsiella	344	27	87.1	620	2	0628B3_CAEBR	0628B3_caenorthabdi
272	27	87.1	464	2	Q8KP24_KLEAE	Q8KP24_klebsiella	345	27	87.1	620	2	Q2UPV4_ASPOR	Q2UPV4_aspergillus
273	27	87.1	465	1	ARB8_ERMCH	Q6D517_erynia_chr	346	27	87.1	629	2	Q8NNV7_CORGL	Q8NNV7_corynebacte
274	27	87.1	467	2	Q9GPI3_LEIIN	Q9GPI3_leishmania	347	27	87.1	638	2	Q7N903_PHOLL	Q7N903_photobactadu
275	27	87.1	468	2	Q6QGV5_PSECC	Q6QGV5_pseudobacter	348	27	87.1	642	2	Q67OV8_SYWTH	Q67OV8_symbiobacte
276	27	87.1	472	2	Q2XCE9_PSEPU	Q2XCE9_pseudomonas	349	27	87.1	647	1	S23A2_MOUSE	09EP94_mus_musculu
277	27	87.1	472	2	Q88N24_PSEPK	Q88N24_pseudomonas	350	27	87.1	650	1	S23A2_HUMAN	080Y23_mus_musculu
278	27	87.1	473	2	Q9Z664_ZYMMO	Q9Z664_zymomonas_m	351	27	87.1	651	2	Q97576_PIG	Q97576_sus_scrofa
279	27	87.1	473	2	Q3KJF6_PSEPF	Q3KJF6_pseudomonas	352	27	87.1	660	1	AT12_VZVD	0742D1_MYCPA
280	27	87.1	473	2	Q4K6Z6_PSEPF	Q4K6Z6_pseudomonas	353	27	87.1	661	2	Q2B152_HMY3	Q2B152_human herpes
281	27	87.1	475	2	Q5N1M2_ZYMMO	Q5N1M2_zymomonas_m	354	27	87.1	661	2	Q2B152_HMY3	Q2B152_human herpes
282	27	87.1	478	2	Q5BPM0_EMENT	Q5BPM0_aspergillus	355	27	87.1	661	2	Q6QCP3_HMY3	Q6QCP3_human herpes
283	27	87.1	478	2	Q9A9Y9_CAUCR	Q9A9Y9_caulobacter	356	27	87.1	661	2	Q6QCP3_HMY3	Q6QCP3_human herpes
284	27	87.1	481	2	Q41607_GIBEX	Q41607_gibberella	357	27	87.1	672	1	Y984_MYCBO	P09264_saricella-z
285	27	87.1	483	2	Q48G57_PSE14	Q48G57_pseudomonas	358	27	87.1	672	1	Y984_MYCBO	Q95C91_homo_sapien
286	27	87.1	483	2	Q4ZOK9_PSEU2	Q4ZOK9_pseudomonas	359	27	87.1	675	2	Q9BT91_HUMAN	Q9BT91_homo_sapien
287	27	87.1	483	2	Q885G3_PSEBM	Q885G3_pseudomonas	360	27	87.1	675	2	Q58EB8_XENLA	Q58EB8_xenopus_lae
288	27	87.1	484	2	Q7Z9M2_TTRRE	Q7Z9M2_trichoderma	361	27	87.1	680	1	DCP_SALTU	P27236_salmoneila
289	27	87.1	488	2	Q9AEN6_ACTNA	Q9AEN6_actinomyces	362	27	87.1	680	2	Q57FC6_SALCH	Q57FC6_salmoneila
290	27	87.1	488	2	Q4SU72_TETNG	Q4SU72_tetradon n	363	27	87.1	680	2	Q5PHG4_SALPA	Q5PHG4_salmoneila
291	27	87.1	492	2	Q39B85_BURS3	Q39B85_burholderi	364	27	87.1	680	2	Q8Z627_SALTU	Q8Z627_salmoneila
292	27	87.1	494	2	Q3F322_9BURK	Q3F322_burholderi	365	27	87.1	687	2	Q346T5_RHOPA	Q346T5_rhodopseudo
293	27	87.1	494	2	Q450X1_9BURK	Q450X1_burholderi	366	27	87.1	687	2	Q35N66_9BRAD	Q35N66_bradyrhizob
294	27	87.1	494	2	Q4B8B6_BURVI	Q4B8B6_burholderi	367	27	87.1	687	2	Q35YR7_RHOPA	Q35YR7_rhodopseudo
295	27	87.1	494	2	Q4BTR1_BURVI	Q4BTR1_burholderi	368	27	87.1	687	2	Q37L11_RHOPA	Q37L11_rhodopseudo
296	27	87.1	494	2	Q4LMW0_9BURK	Q4LMW0_burholderi	369	27	87.1	687	2	Q3ZPC5_NITWA	Q3ZPC5_nitrobacter
297	27	87.1	494	2	Q39P92_BURS3	Q39P92_burholderi	370	27	87.1	687	2	Q3SPA9_NITWA	Q3SPA9_nitrobacter
298	27	87.1	495	2	Q454S8_9BURK	Q454S8_burholderi	371	27	87.1	687	2	Q3JG96_BURP1	Q3JG96_burholderi
299	27	87.1	495	2	Q4LQW2_9BURK	Q4LQW2_burholderi	372	27	87.1	687	2	Q2J0W1_RHOPA	Q2J0W1_rhodopseudo
300	27	87.1	496	2	Q2SMW0_BURTH	Q2SMW0_burholderi	373	27	87.1	687	2	Q6NNA3_RHOPA	Q6NNA3_rhodopseudo
301	27	87.1	497	2	Q6MYG5_ASPFU	Q6MYG5_aspergillus	374	27	87.1	687	2	Q8S5D8_BRADA	Q8S5D8_bradyrhizob
302	27	87.1	497	2	Q4WRG4_ASPFU	Q4WRG4_aspergillus	375	27	87.1	717	2	Q4SDQ2_TERNG	Q4SDQ2_tetradon n
303	27	87.1	500	2	Q88Y80_LACPL	Q88Y80_lactobacill	376	27	87.1	726	2	Q3JUPV5_BURP1	Q3JUPV5_burholderi
304	27	87.1	502	2	Q82GV1_STRPW	Q82GV1_streptomyce	377	27	87.1	735	2	Q3GLZ1_9GAMM	Q3GLZ1_psychrobact
305	27	87.1	510	2	Q57SG3_SALCH	Q57SG3_salmoneila	378	27	87.1	737	1	AMY1_AEDAE	P53354_aedes_aegyp
306	27	87.1	513	2	Q3F681_9BURK	Q3F681_burholderi	379	27	87.1	737	2	Q02413_AEDAE	Q02413_aedes_aegyp
307	27	87.1	524	2	Q87143_VIBPA	Q87143_vibri	380	27	87.1	738	2	Q4B217_9BURK	Q4B217_bacterales
308	27	87.1	525	2	Q3WZEB_9ACTN	Q3WZEB_rubrobacter	381	27	87.1	752	2	Q3PRT5_PARDE	Q3PRT5_pareicoccus
309	27	87.1	530	2	Q5HKM4_STABO	Q5HKM4_staphylococ	382	27	87.1	761	2	Q34DB7_RHOPA	Q34DB7_rhodopseudo
310	27	87.1	530	2	Q8CQ99_STARS	Q8CQ99_staphylococ	383	27	87.1	762	2	Q37FJ0_RHOPA	Q37FJ0_rhodopseudo
311	27	87.1	536	2	Q873X2_FUSSP	Q873X2_fusarium sp	384	27	87.1	762	2	Q21W27_RHOPA	Q21W27_rhodopseudo
312	27	87.1	542	2	Q8U127_FUSSP	Q8U127_fusarium sp	385	27	87.1	763	2	Q36VU4_RHOPA	Q36VU4_rhodopseudo
313	27	87.1	542	2	Q96VQ9_FUSSP	Q96VQ9_fusarium sp	386	27	87.1	763	2	Q6N6M1_RHOPA	Q6N6M1_rhodopseudo
314	27	87.1	543	2	Q810P0_CAEBL	Q810P0_caenorthabdi	387	27	87.1	764	2	Q3P098_NITWA	Q3P098_nitrobacter
315	27	87.1	544	2	Q4UCP8_THEAN	Q4UCP8_theileria a	388	27	87.1	766	2	Q3S8N4_NITWA	Q3S8N4_nitrobacter
316	27	87.1	547	2	Q3PVG4_NITWA	Q3PVG4_xenopus lae	389	27	87.1	784	2	Q3SEBP6_9BRAD	Q3SEBP6_bradyrhizob
317	27	87.1	549	2	Q5XGN4_XENLA	Q5XGN4_xenopus lae	390	27	87.1	799	2	Q6ZCR4_ORYSA	Q6ZCR4_oryza_sativ
318	27	87.1	557	2	Q4NSC9_ASPFU	Q4NSC9_aspergillus	391	27	87.1	848	2	Q6MPE2_BDRBA	Q6MPE2_bdellovibri
319	27	87.1	560	2	Q2UCU1_ASPOR	Q2UCU1_aspergillus	392	27	87.1	848	2	Q891Q4_BRADA	Q891Q4_bradyrhizob
320	27	87.1	566	1	CPB2_CAEBR	Q6E313_caenorthabdi	393	27	87.1	899	2	Q3XJ30_9PROT	Q3XJ30_magnetococ
321	27	87.1	571	1	CPB2_CAEBR	Q6E312_caenorthabdi	394	27	87.1	963	2	Q5S071_THET8	Q5S071_thermus the
322	27	87.1	575	2	Q6ZRB0_HUMAN	Q6ZRB0_homo sapien	395	27	87.1	963	2	Q72UJ4_THBT2	Q72UJ4_thermus the
323	27	87.1	579	2	Q9Z7V7_CHLBN	Q9Z7V7_chlamydia p	396	27	87.1	1014	2	Q2IPV0_9DELT	Q2IPV0_aeaeomyxob

397	27	87.1	1130	2	Q4SVS4_TETNG	Q4svs4 tetradon n
398	27	87.1	1170	2	Q2T4P2_BURTH	Q2t4p2 burkholderi
399	27	87.1	1240	2	Q38B4_9TRYF	Q38b4 trypanosoma
400	27	87.1	1377	2	Q9P2A8_HUMAN	Q9p2a8 homo sapien
401	27	87.1	1467	2	Q4RMJ3_TETNG	Q4rmj3 tetradon n
402	27	87.1	1481	2	Q9U107_CAEEL	Q9u107 caenorhabdi
403	27	87.1	1481	2	Q8CFQ3_MOUSE	Q8cfq3 mus musculu
404	27	87.1	1481	2	Q3ULE8_MOUSE	Q3ule8 mus musculu
405	27	87.1	1500	2	Q80TX8_MOUSE	Q80tx8 mus musculu
406	27	87.1	1521	2	Q60306_HUMAN	Q60306 homo sapien
407	27	87.1	1542	2	Q2SHZ2_9GAWM	Q2shz2 habella che
408	27	87.1	1632	2	Q93593_CAEEL	Q93593 caenorhabdi
409	27	87.1	1636	2	Q40Y08_KINRA	Q40y08 kinetococcus
410	27	87.1	1833	2	Q57086_9TRYF	Q57086 trypanosoma
411	27	87.1	1954	2	Q4WKS1_ASPFU	Q4wks1 aspergillus
412	27	87.1	2006	2	Q5BGD9_EMENT	Q5bgd9 aspergillus
413	27	87.1	2089	2	Q4D889_TRYCR	Q4d889 trypanosoma
414	27	87.1	2126	2	Q6P4S8_MOUSE	Q6p4s8 mus musculu
415	27	87.1	2798	2	Q4DMW7_TRYCR	Q4dmw7 trypanosoma
416	27	87.1	2982	2	Q4RXP0_TETNG	Q4rxp0 tetradon n
417	27	87.1	3167	2	Q7Q087_GIALA	Q7q087 giardia lam
418	26	83.9	68	2	Q8R728_THETN	Q8r728 thermoaenar
419	26	83.9	77	2	Q2VZM8_MAGSA	Q2vzm8 magnetospir
420	26	83.9	80	2	Q9KRZ6_VIBCH	Q9krz6 vibrio chol
421	26	83.9	84	2	Q5BT57_SCHUA	Q5bt57 schistosoma
422	26	83.9	98	2	Q58PS6_9PROT	Q58ps6 uncultured
423	26	83.9	102	1	Y116_YEAST	P40503 saccharomyc
424	26	83.9	102	2	Q7W3B4_BORPA	Q7w3b4 bordetella
425	26	83.9	105	2	Q3AM77_SYNSC	Q3am77 synecchococ
426	26	83.9	105	2	Q44SD5_CHILT	Q44sd5 chlorobium
427	26	83.9	107	2	Q6Z565_ORYSA	Q6z565 oryza sativ
428	26	83.9	107	2	Q9R6Q7_PROMT	Q9r6q7 proteus mix
429	26	83.9	112	2	Q3X4U8_9ACTN	Q3x4u8 rubrobacter
430	26	83.9	114	2	Q9SFZ6_ARATH	Q9sfz6 arabidopsis
431	26	83.9	116	2	Q3RRU5_RALME	Q3rru5 ralsconia m
432	26	83.9	116	2	Q4N1J9_9MICC	Q4n1j9 arthrobacte
433	26	83.9	119	2	Q2XVU1_9CAUD	Q2xvu1 bacterioph
434	26	83.9	119	2	Q3HLE6_9CAUD	Q3hle6 bacillus an
435	26	83.9	119	2	Q2LIC3_9CAUD	Q2lic3 bacillus an
436	26	83.9	119	2	Q2LH6_9CAUD	Q2lih6 bacillus an
437	26	83.9	119	2	Q3H1L0_9CAUD	Q3h1l0 bacillus an
438	26	83.9	119	2	Q218R3_9CAUD	Q218r3 bacillus an
439	26	83.9	121	2	Q3D1N5_STRAG	Q3d1n5 streptococ
440	26	83.9	121	2	Q3DLF5_STRAG	Q3dlf5 streptococ
441	26	83.9	121	2	Q54884_STRPN	Q54884 streptococ
442	26	83.9	121	2	Q8DZ66_STRAS	Q8dz66 streptococ
443	26	83.9	121	2	Q8E4R2_STRRA3	Q8e4r2 streptococ
444	26	83.9	121	2	Q97QY7_STRPN	Q97qy7 streptococ
445	26	83.9	131	2	Q3VL18_9CHLB	Q3vl18 pelodictyon
446	26	83.9	131	2	Q3ASB5_CHLCH	Q3asb5 chlorobium
447	26	83.9	136	2	Q43GL7_9CHLB	Q43gl7 chlorobium
448	26	83.9	138	2	Q3B6N1_PELLD	Q3b6n1 pelodictyon
449	26	83.9	139	2	Q43H29_9CHLB	Q43h29 chlorobium
450	26	83.9	147	2	Q8J1L4_9CAUD	Q8j1l4 virus plich
451	26	83.9	151	2	Q2XG16_PSEPU	Q2xg16 pseudomonas
452	26	83.9	151	2	Q88L75_PSEPK	Q88l75 pseudomonas
453	26	83.9	155	2	Q413G9_KINRA	Q413g9 kinetococcus
454	26	83.9	156	2	Q4H2Y6_CIOIN	Q4h2y6 clona intes
455	26	83.9	156	2	Q4C9K4_CROWT	Q4c9k4 crocosphaer
456	26	83.9	156	2	Q4M540_CHITE	Q4m540 chlorosoma
457	26	83.9	157	2	Q4DK86_TRYCR	Q4dk86 trypanosoma
458	26	83.9	160	2	Q4KHV0_PSEFS	Q4khv0 pseudomonas
459	26	83.9	169	2	Q3X4I3_9ACTN	Q3x4i3 rubrobacter
460	26	83.9	174	1	YDSA_SCHHO	Q4185 pschistosch
461	26	83.9	174	1	Q3CVD7_ALTTAT	Q3cvt7 pseudocall
462	26	83.9	175	2	Q4F6C0_IPOBA	Q4f6c0 ipomea bat
463	26	83.9	178	2	Q3X4J5_9ACTN	Q3x4j5 rubrobacter
464	26	83.9	179	2	Q5F6Y7_NEIG1	Q5f6y7 nisseeria g
465	26	83.9	184	2	Q46PY1_RALEJ	Q46py1 ralsconia g
466	26	83.9	188	2	Q72G50_DESVH	Q72g50 desulfovibr
467	26	83.9	189	2	Q4MTA2_BACCE	Q4mta2 bacillus ce
468	26	83.9	199	2	Q97B39_THEVO	Q97b39 thermoplasma
469	26	83.9	200	2	Q5C2N9_SCHUA	Q5c2n9 schistosoma

470	26	83.9	205	2	Q7NCK8_GLOVI	Q7nck8 gloebacter
471	26	83.9	210	2	Q9H6X7_HUMAN	Q9h6x7 homo sapien
472	26	83.9	212	2	Q67WM8_ORYSA	Q67wm8 oryza sativ
473	26	83.9	212	2	Q89WM0_BRATA	Q89wm0 bradyrhizob
474	26	83.9	217	2	Q7FAT5_ORYSA	Q7fat5 oryza sativ
475	26	83.9	229	2	Q8W1J2_9CHLO	Q8w1j2 chloregoniu
476	26	83.9	229	2	Q84FS6_9BACT	Q84fs6 bacillus sp
477	26	83.9	229	2	Q9L542_9BACT	Q9l542 bacillus sp
478	26	83.9	230	2	Q3J287_RHOS4	Q3j287 rhodobacter
479	26	83.9	230	2	Q9R699_9RHIZ	Q9r699 agrobacteri
480	26	83.9	230	2	Q9R716_9RHIZ	Q9r716 agrobacteri
481	26	83.9	231	2	Q9WME4_9RHIZ	Q9wme4 agrobacteri
482	26	83.9	231	2	Q8UEA7_9AGRT5	Q8uea7 agrobacteri
483	26	83.9	235	2	Q7MW21_PORCI	Q7mw21 porphyromon
484	26	83.9	237	2	Q3WOK7_9ACTO	Q3wok7 frackia sp.
485	26	83.9	238	2	Q5AVB1_EMENT	Q5avb1 aspergillus
486	26	83.9	238	2	Q3AMV7_SYNSC	Q3amv7 synecchococ
487	26	83.9	240	2	Q9PCD9_STRGO	Q9pcd9 streptomyc
488	26	83.9	241	2	Q8Z6R4_STRAM	Q8z6r4 streptomyc
489	26	83.9	246	2	Q4DC54_TRYCR	Q4dc54 trypanosoma
490	26	83.9	247	2	Q5KME0_GEOXA	Q5kme0 geobacillus
491	26	83.9	248	2	Q6WH44_BPKV4	Q6wh44 bacterioph
492	26	83.9	250	2	Q8N1Z8_EMENT	Q8n1z8 emericella
493	26	83.9	250	2	Q5B3H5_EMENT	Q5b3h5 aspergillus
494	26	83.9	250	2	Q98PG7_MYCPU	Q98pg7 mycoplasma
495	26	83.9	252	1	PIGL_HUMAN	Q9y2b2 homo sapien
496	26	83.9	252	2	Q5SX19_MOUSE	Q5sx19 mus musculu
497	26	83.9	255	2	Q8CIL4_MOUSE	Q8cil4 mus musculu
498	26	83.9	259	2	Q4CN61_TRYCR	Q4cn61 trypanosoma
499	26	83.9	259	2	Q3X1H3_9ACTN	Q3x1h3 rubrobacter
500	26	83.9	261	2	O17262_CAEEL	O17262 caenorhabdi

ALIGNMENTS

RESULT 1
 Q2SEI3_9GAWM PRELIMINARY; PRT; 324 AA.
 ID Q2SEI3_9GAWM
 AC Q2SEI3;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Hypothetical protein.
 GN ORFNames=HCH_04234;
 OS *Hahella chejuensis* KCTC 2396.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
 OC *Hahellaceae*; *Hahella*.
 OX NCBI_TaxID=349521;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=KCTC 2396;
 RX PubMed=16352867; DOI=10.1093/nar/gki1016;
 RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
 RA Park H.-S., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
 RA Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
 RT "Genomic blueprint of *Hahella chejuensis*, a marine microbe producing
 an alginate agent.";
 RL Nucleic Acids Res. 33:7066-7073(2005).
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC EMBL; CP000155; ABC0941.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 324 AA; 36310 MM; E523A970CF11A081 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 1 FSRYAR 6
 |||||

DB 125 FSRYAR 130

RESULT 2

ID 0709K9 ANOGA PRELIMINARY; PRT; 338 AA.

AC 0709K9;

DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.

DT 07-DEC-2004, sequence version 2.

DT 07-FEB-2006, entry version 7.

DE ENSANGP0000015636 (Fragment).

GN ORFNames=ENSANG00000013147;

OS Anopheles gambiae str. PST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;

OC Anophelinae; Anopheles.

OX NCBI_TaxID=180454;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST.

RG The Anopheles gambiae Sequence Committee;

RT "Anopheles gambiae re-annotation.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST.

RG The Anopheles gambiae Sequence Committee;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC -----

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CC -----

DR EMBL: AAB01008900, BAA09433.2; -, Genomic_DNA.

DR NON_TER 1

FT SEQUENCE 338 AA; 39557 MW; B6534CB28EFA3737 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 338;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6

DB 277 FSRYAR 282

RESULT 3

PAAB_ECOLI

ID PAAB_ECOLI STANDARD; PRT; 356 AA.

AC P76081; O53013; P77233;

DT 27-APR-2001, integrated into UniProtKB/Swiss-Prot.

DT 01-FEB-1997, sequence version 1.

DT 07-MAR-2006, entry version 56.

DE Probable phenylacetic acid degradation NADH oxidoreductase paab

DE (EC 1.-.-.-).

GN Name=paab; OrderedLocustNames=b1392;

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC STRAIN=M / ATCC 11105;

RX MEDLINE=98421522; PubMed=9748275; DOI=10.1074/jbc.273.40.25974;

RA Parrander A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,

RA Garcia J.L., Diaz E.;

RT "Catabolism of phenylacetic acid in Escherichia coli. Characterization

RT of a new aerobic hybrid pathway.";

RL J. Biol. Chem. 273:25974-25986(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12;

RX MEDLINE=97251357; PubMed=9097039; DOI=10.1093/dnares/3.6.363;

RA Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,

RA Sempel G., Seki Y., Sivasubaram S., Tagami H., Takeda J.,

RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horitsu T.;

RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 28.0-40.1 min region on the linkage map.";

RL DNA Res. 3:363-377(1996).

RN [4]

RP TRANSCRIPTIONAL REGULATION.

RX MEDLINE=20229831; PubMed=10766858; DOI=10.1074/jbc.275.16.12214;

RA Parrander A., Garcia J.L., Diaz E.;

RT "Transcriptional regulation of the divergent paa catabolic operons for

RT phenylacetic acid degradation in Escherichia coli.";

RL J. Biol. Chem. 275:12214-12222(2000).

CC -1- FUNCTION: May be part of a multicomponent oxygenase involved in

CC phenylacetyl-CoA hydroxylation.

CC -1- COFACTOR: Binds 1 2Fe-2S cluster (By similarity).

CC -1- PATHWAY: Phenylacetic acid aerobic catabolism.

CC -1- INDUCTION: Activated by cAMP receptor protein (CRP) and

CC integration host factor (IHF). Inhibited by paaX.

CC -1- SIMILARITY: In the N-terminal section, belongs to the FAD-binding

CC oxidoreductase type 6 family.

CC -1- SIMILARITY: Contains 1 2Fe-2S ferredoxin-type domain.

CC -----

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CC -----

DR EMBL: X97452; CA66094.1; -, Genomic_DNA.

DR EMBL: U00096; AAC74474.1; -, Genomic_DNA.

DR EMBL: D90777; BAA14998.1; ALT_INIT; Genomic_DNA.

DR EMBL: D90778; BAA15003.1; ALT_INIT; Genomic_DNA.

DR PIR: C64890; C64890.

DR HSSP: P06543; 1J7B.

DR GenomeReviews: U00096_GR; b1392.

DR Echobase; EB3502; -.

DR EcoGene; EGI3739; paaB.

DR BioCyc; EcoCyc:G6713-MONOMER; -.

DR LinkHub; P76081; -.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR01041; Ferredoxin.

DR InterPro; IPR012675; Ferredoxin fold.

DR InterPro; IPR001709; FPN_cye_redctse.

DR InterPro; IPR008333; Oxred_FAD_bd.

DR InterPro; IPR001433; Oxred_FAD_NAD_bd.

DR InterPro; IPR011884; PA_CoA_Oase5.

DR InterPro; IPR001221; Phe_hydroxylase.

DR Pfam; PF00970; FAD_binding_6; 1.

DR Pfam; PF00111; Fer2; 1.

DR Pfam; PF00175; NAD_binding_1; 1.

DR PRINTS; PR00371; FENCR.

DR PRINTS; PR00410; PHEHYDLASE.

DR TIGRFAMs; TIGR02160; PA_CoA_Oxy5; 1.

DR PROSITE; PS1085; 2FE2S_FER_2; 1.

DR PROSITE; PS00197; 2FE2S_FER_1; 1.

DR 2Fe-2S; Complete proteome: Electron transport; FAD; Flavoprotein;

KW Iron; Iron-sulfur; Metal-binding; NAD; Oxidoreductase; Transport.

FT CHAIN 1 356

FT NADH oxidoreductase paaB.

```

FT DOMAIN 262 354 /FTId=PRO_0000058163.
FT REGION 112 228 2Fe-2S ferredoxin-type.
FT METAL 299 299 Oxidoreductase (potential).
FT METAL 304 304 Iron-sulfur (2Fe-2S) (By similarity).
FT METAL 307 307 Iron-sulfur (2Fe-2S) (By similarity).
FT METAL 337 337 Iron-sulfur (2Fe-2S) (By similarity).
FT VARIANT 14 14 S -> P (in strain: W).
FT VARIANT 169 169 P -> S (in strain: W).
FT VARIANT 224 227 DAET -> ETEA (in strain: W).
SQ SEQUENCE 356 AA; 39320 MW; D719C1CA81DA5FFA CRC64;

Query Match 100.0%; Score 31; DB 1; Length 356;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 80 FSRYPAR 85

RESULT 4
MURG_CHLPP STANDARD; PRT; 357 AA.
AC Q92702; Q9J027;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1999, sequence version 1.
DT 07-MAR-2006, entry version 36.
DE UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide)
DE pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
DE (EC 2.4.1.22) (Undecaprenyl-PP-murNac-pentapeptide-UDPglcNAc
DE transferase).
GN Name=murg; OrderedLocustNames=CPN0904, CP0962, CPB0936;
OS Chlamydia pneumoniae (Chlamydiophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiophila.
OX NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=J138;
RA MEDLINE=9920606; PubMed=10192388; DOI=10.1038/7716;
RA Kaiman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.",
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AR39;
RA MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utecherback T.R., Berry K.J.,
RA Bass S., Linkey K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Ginn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McLacty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mohn and Chlamydia
RT pneumoniae AR39.",
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=J138;
RA MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.",
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.",
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

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CC -1- FUNCTION: Cell wall formation. Catalyzes the transfer of a GlcNAc
CC subunit on undecaprenyl-pyrophosphoryl-murNac-pentapeptide (lipid
CC intermediate II) to form undecaprenyl-pyrophosphoryl-murNac-
CC (pentapeptide)GlcNAc (lipid intermediate II) (By similarity).
CC -1- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oyl-D-Ala-
CC gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP +
CC GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-
CC diphosphoundecaprenol.
CC -1- PATHWAY: Peptidoglycan biosynthesis; last step.
CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; peripheral
CC membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the glycosyltransferase 28 family. MurG
CC subfamily.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL, AE001670; MAD19042.1; -; Genomic DNA.
CC EMBL, AE002254; AAP38742.1; -; Genomic DNA.
CC EMBL, BA000008; BAA99112.1; -; Genomic DNA.
CC EMBL, AE017160; AAP98865.1; ALT_INIT; Genomic DNA.
CC PIR, C72022; C72022.
CC PIR, F86603; F86603.
CC DR GenomeReviews; AE002161_GR; CP0962.
CC DR GenomeReviews; AE009440_GR; CPB0936.
CC DR GenomeReviews; AE001363_GR; CPN0904.
CC DR GenomeReviews; BA000008_GR; murg.
CC DR TIGR; CP0962; -.
CC DR BioCyc; CPN115711.CP0962-MONOMER; -.
CC DR BioCyc; CPN115713.CP0904-MONOMER; -.
CC DR BioCyc; CPN138677.CP0904-MONOMER; -.
CC DR BioCyc; CPN182082.CPB0936-MONOMER; -.
CC DR HAMAP; MF_00033; -; 1.
CC DR InterPro; IPR007235; Glyco_tran_28_C.
CC DR InterPro; IPR004276; Glyco_trans_26.
CC DR InterPro; IPR006009; Murg.
CC DR Pfam; PF04101; Glyco_tran_28_C; 1.
CC DR Pfam; PF03033; Glyco_transf_28; 1.
CC DR TIGRFAMs; TIGR01133; murg; 1.
CC KM Cell cycle; Cell division; Cell shape; Cell wall; Complete proteome;
CC Glycosyltransferase; Inner membrane; Membrane;
CC Peptidoglycan synthesis; Transferase.
CC KEGG CHAIN 1 357
CC FT
CC FT
CC FT
CC SQ SEQUENCE 357 AA; 39420 MW; DEB8350CF168BC42 CRC64;
CC
CC Query Match 100.0%; Score 31; DB 1; Length 357;
CC Best Local Similarity 100.0%; Pred. No. 91;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 135 FSRYPAR 140

RESULT 5
Q5SMX2_ORYSA PRELIMINARY; PRT; 412 AA.
ID Q5SMX2_ORYSA
AC Q5SMX2;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Basic helix-loop-helix protein-like.
GN Name=P04980.1.25;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPF clade;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2237376; Pubmed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Katsamori H.,
RA Nagakawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijikata S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
RA Karaawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Showura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Maki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RL "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -----
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CC -----
DR EMBL; AP003417; BAD72431.1; -; Genomic_DNA.
CC
DR Gramene; Q5SMX2; -.
CC
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0030528; F:transcription regulator activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR015598; HLH_DNA_bd.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS50868; HLH; 1.
DR SQ SEQUENCE 412 AA; 43709 MW; 644AA46084EB40B2 CRC64;
QY 1 FSRYPAR 6
Db 117 FSRYPAR 122

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DR EMBL; BA000012; BAB48618.1; -; Genomic_DNA.
DR BioCyc; MLOT381; ML1183-MONOMER; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR011761; ATP_GASP.
DR PROSITE; PS50975; ATP_GASP; 1.
KM ATP-binding; Complete proteome; Nucleotide-binding.
SQ SEQUENCE 427 AA; 46722 MW; F4435AC1EDC7F645 CRC64;
QY 1 FSRYPAR 6
Db 53 FSRYPAR 58

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Query Match 100.0%; Score 31; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
ID Q5J1L5 ALCEFA PRELIMINARY; PRT; 432 AA.
AC Q5J1L5;
DT 15-FEB-2005; Integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005; sequence version 1.
DT 07-FEB-2006; entry version 4.
DE Phor.
GN Name=phor;
OS Alcaligenes faecalis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OC NCBI_TaxID=511;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WM2072;
RX Pubmed=15640200; DOI=10.1128/AEM.71.1.290-296.2005;
RA Wilson M.M., Metcalf W.W.;
RT "Genetic Diversity and Horizontal Transfer of Genes Involved in
RT Oxidation of Reduced Phosphorus Compounds by Alcaligenes faecalis
RT WM2072.";
RL Appl. Environ. Microbiol. 71:290-296(2005).
RL [2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WM2072;
RA Wilson M., Metcalf W.W.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY548383; AAT12782.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation system (p...); IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
DR InterPro; IPR004358; ATP_bd_ATPase.
DR InterPro; IPR003594; ATP_bd_ATPase.
DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR008358; Lantibiot_regn.
DR Pfam; PF02512; HATPase_c; 1.
DR Pfam; PF00512; HATPase_c; 1.
DR PRINTS; PR00344; BCTRSENSOR.
DR PRINTS; PR01780; LANTIREGPRON.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HSKA; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR SQ SEQUENCE 432 AA; 48532 MW; 74A8B90180BFA76 CRC64;
QY 1 FSRYPAR 6
Db 53 FSRYPAR 58

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Query Match 100.0%; Score 31; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FSRYAR 6
Db 147 FSRYAR 152

RESULT 8
Q62CX5 BURMA PRELIMINARY; PRT; 447 AA.
ID 062CX5 BURMA PRELIMINARY; PRT; 447 AA.
AC 062CX5;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Amino acid permealase.
GN OrderedLocustNames=BMAA0717;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Niernan W.C., Deshaizer D., Kim H.S., Tectelin H., Nelson K.E.,
RA Feldblum T.V., Ulrich R.L., Romning C.M., Brinton L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dintirov G., Dodson R.J.,
RA Durkin A.S., Gwin M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarría S., Selengut J., Shambin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
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CC -----
DR EMBL; CP000011; AAU46888.1; -; Genomic DNA.
DR TIGR; BMAA0717; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004840; AAC permease.
DR InterPro; IPR004841; Permease region.
DR PANTHER; PTHR11785; AA/rel_permease1; 1.
DR Pfam; PF00324; AA_permease1; 1.
DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
DR Complete proteome.
SQ SEQUENCE 447 AA; 48683 MW; A209ED83F6C1D427 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FSRYAR 6
Db 76 FSRYAR 81

RESULT 9
Q45AY3 BURK PRELIMINARY; PRT; 460 AA.
ID Q45AY3 BURK PRELIMINARY; PRT; 460 AA.
AC Q45AY3;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Amino acid permealase-associated region.
GN ORFNames=BcendraFT_5191;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

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OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Plick S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Lartner F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054." (JUN-2005) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AAH10100004; EAM13792.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004840; AAC permease.
DR Pfam; PF00324; AA_permease1; 1.
DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
DR Complete proteome.
SQ SEQUENCE 460 AA; 49648 MW; 68760B59F03369D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FSRYAR 6
Db 76 FSRYAR 81

RESULT 10
Q4LT22 BURK PRELIMINARY; PRT; 460 AA.
ID Q4LT22 BURK PRELIMINARY; PRT; 460 AA.
AC Q4LT22;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Amino acid permealase-associated region.
GN ORFNames=Bcen2424DRAFT_4131;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Plick S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);

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RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RL HIT2424."
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAHL0100016; EML19436.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004840; AAC_permease.
DR PANTHER; PTHR11785; AA/rel_permease1; 1.
DR Pfam; PF00324; AA_permease; 1.
DR PROSITE; PS00218; AMINO ACID_PERMEASE_1; 1.
SQ SEQUENCE 460 AA; 49648 MW; 68780B9E9F03369D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 76 FSRYAR 81

RESULT 11
Q395V1 BUR53 PRELIMINARY; PRT; 460 AA.
AC Q395V1
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Amino acid transporter.
GN OrderedLocustNames=Bcep18194_B1646;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute.
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,
RA Hammon N., Israel S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Verges L., Schmitt J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of chromosome 2 of Burkholderia sp. 383."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000152; ABB11760.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:00016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
KW Complete proteome.
SQ SEQUENCE 460 AA; 49728 MW; D6BBA9AF2CD5155 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 FSRYAR 6
Db 76 FSRYAR 81

RESULT 12
Q2T424 BURTH PRELIMINARY; PRT; 461 AA.
ID Q2T424 BURTH
AC Q2T424
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Amino acid permease.
GN ORFNames=BTH_11560;
OS Burkholderia thailandensis B264.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=271848;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E264;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Palmer N., Dodson R.,
RA Hickey B.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D.,
RA Peterson J., Kervavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van-Vugt R., Adams M.D., Gocayne J.D., Weidman C., Ullrich T.,
RA Wathey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C.,
RA Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O.,
RA Venter J.C.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000085; ABC5479.1; -; Genomic DNA.
DR SEQUENCE 461 AA; 49957 MW; 7F1195E772F28B65 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 76 FSRYAR 81

RESULT 13
Q3JFR3 BURP1 PRELIMINARY; PRT; 461 AA.
ID Q3JFR3 BURP1
AC Q3JFR3
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Amino acid permease.
GN Name=proX; OrderedLocustNames=BURP51710B_A2440;
OS Burkholderia pseudomallei (strain 1710B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=320372;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP Moore D.E., Nieman W.C.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000125; ABA52590.1; -; Genomic DNA.
DR TIGR; BURP51710B_A2440; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:00016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.

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DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.
DR Pfam: PF00324; AA_permease_1.1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1.1.
DR Complete proteome.
SQ SEQUENCE 461 AA; 50051 MW; 2DBA117A4942B62E CRC64;

Query Match 100.0%; Score 31; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
DB 76 FSRYPAR 61

RESULT 14
O63M15 BURPS PRELIMINARY; PRT; 461 AA.
ID O63M15 BURPS
AC O63M15
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Putative proline-specific permease.
GN Name=ProY; OrderedLocustNames=BPS0845;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN 1
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Fittell R.W., Peacock S.O., Cerdano-Tarraga A.-M.,
RA Aktins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosser B., Davis P., Desnazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jørgels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songswilvit S., Stevens K., Tumapa S., Vesaratchavee M.,
RA Whitehead S., Yeates C., Barrett B.G., Oyston P.C.F., Parkhill J.;
RA "Genomic plasticity of the causative agent of melioidosis,"
RT Burkholderia pseudomallei";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
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CC -----
EMBL: BX51966; CAH8307.1; Genomic_DNA.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.
DR PANTHER: PTHR11785; AA/rel_permease1.1.
DR Pfam: PF00324; AA_permease_1.1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1.1.
DR Complete proteome.
SQ SEQUENCE 461 AA; 50021 MW; D7BAE75BB033B15F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
DB 76 FSRYPAR 61

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DB 76 FSRYPAR 61

RESULT 15
O34618 BACSU PRELIMINARY; PRT; 463 AA.
ID O34618 BACSU
AC O34618; Q795P5;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Amino acid transporter (YtnA protein).
GN Name=YtnA; OrderedLocustNames=BSU30530;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN 1
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98048467; PubMed=9387221;
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.-D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rnm-dnaB region.";
RL Microbiology 143:3431-3441(1997).
RN 2
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertaino M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Ehtian K.-D., Eyrington J., Fabre C., Ferrati E., Fougier D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.-Y., Glaeser P., Goffeau A., Goldlighty E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haeleth J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.-F., Itaya M.,
RA Jones L.W., Joris B., Karamata D., Kasaara Y., Kleier-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pulic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadleir Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Seifone F., Sekiguchi J., Sekowska A., Serr S.J., Serron P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vessaretti A., Viari A., Wambuit S., Wedler H., Wedler H.,
RA Weitzneger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasunoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA Yoshikawa H., Zanchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
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CC -----
EMBL: AF008220; AAC00244.1; Genomic_DNA.
DR EMBL: Z99119; CAB15031.1; Genomic_DNA.
DR PIR: C69997; C69997.
DR BioCyc: BSU1423;BSU3048--MONOMER; -.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; F:amino acid-polyamine transporter activity; IEA.

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DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.
DR PANTHER: PTHR11785; AA/rel_permease1; 1.
DR Pfam: PF00324; AA_permease1; 1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1; UNKNOWN_1.
DR Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 463 AA; 50328 MW; B21F9F40AB1C7180 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 76 FSRYPAR 81

RESULT 16
Q2STX5 BURTH PRELIMINARY; PRT; 468 AA.
ID Q2STX5 BURTH PRELIMINARY; PRT; 468 AA.
AC Q2STX5;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Amino acid permease.
GN ORFNames=BTH_13129;
OS Burkholderia thailandensis E264.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=271848;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E264;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Palmer N., Dodson R.,
RA Hickey E.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van-Vugt R., Adams M.D., Gocayne J.D., Weidman J.D., Utechtack T.,
RA Wetthey L., McDonald L., Artach P., Bowman C., Garland S., Fujii C.,
RA Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O.,
RA Venter J.C.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CP000086; ABC38752.1; -; Genomic DNA.
SQ SEQUENCE 468 AA; 50779 MW; A905AA5CB57B7284 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 78 FSRYPAR 83

RESULT 17
Q3JY99 BURP1 PRELIMINARY; PRT; 468 AA.
ID Q3JY99 BURP1 PRELIMINARY; PRT; 468 AA.
AC Q3JY99;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Amino acid permease.
GN OrderedListusNames=BURPS1710b_0036;
OS Burkholderia pseudomallei (strain 1710b).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.

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OX NCBI_TaxID=320372;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Woods D.E., Nielsen W.C.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CP000124; ABAS0182.1; -; Genomic DNA.
DR TIGR: BURPS1710b_0036; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.
DR Pfam: PF00324; AA_permease1; 1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
DR Complete proteome.
SQ SEQUENCE 468 AA; 50889 MW; EBEFA2C3CE681110 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 78 FSRYPAR 83

RESULT 18
Q62G62 BURMA PRELIMINARY; PRT; 468 AA.
ID Q62G62 BURMA PRELIMINARY; PRT; 468 AA.
AC Q62G62;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Amino acid permease.
GN OrderedListusNames=BMA2796;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.040306101;
RA Nielsen W.C., Deshaizer D., Kim H.S., Tetteilin H., Nelson K.E.,
RA Feldblum T.V., Ulrich R.L., Romning C.M., Brinkac L.M.,
RA Dougherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarría S., Selengut J., Shamlin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RL "Structural flexibility in the Burkholderia mallei genome.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
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CC -----
DR EMBL: CP000010; AAU47957.1; -; Genomic DNA.
DR TIGR: BMA2796; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.

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DR PANTHER; PTHR11785; AA/rel_permease; 1.
 DR Pfam; PF00324; AA_permease; 1.
 DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
 KM Complete proteome.
 SQ SEQUENCE 468 AA; 50949 MW; AAEB96964CBBBCB CRC64;

Query Match 100.0%; Score 31; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 |||||
 DB 78 FSRYAR 83

RESULT 19
 ID O63PM6_BURPS PRELIMINARY; PRT; 468 AA.
 AC O63PM6;
 DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Putative amino acid permease.
 GN OrderedLocustNames=BSJ3256;
 OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 OX NCBI_Taxid=28450;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K96243;
 RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
 RA Holden M.T.G., Tilgall R.W., Peacock S.J., Cedeno-Tarrega A.-M.,
 RA Akins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
 RA Bentley S.D., Seabald M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brook K., Brown K.A., Brown N.F., Challis G.L., Chevrech I.,
 RA Chillingworth T., Cronin A., Crosser B., Davis P., Deshaizer D.,
 RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule Z., Price C., Quail M.A.,
 RA Rabbittowtsch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songsvilait S., Stevens K., Tumapa S., Vesaratchavee M.,
 RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 RT Burkholderia pseudomallei.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

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CC EMBL; BX571965; CAH37269.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002293; AA/rel_permease1.
 DR InterPro; IPR004840; AA_permease.
 DR InterPro; IPR004841; Permease region.
 DR PANTHER; PTHR11785; AA/rel_permease; 1.
 DR Pfam; PF00324; AA_permease; 1.
 DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
 KM Complete proteome.
 SQ SEQUENCE 468 AA; 50875 MW; 69E6B0D62E681105 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 |||||
 DB 78 FSRYAR 83

RESULT 20
 ID ASCB_ECOLI STANDARD; PRT; 474 AA.
 AC P24240; P78104; O59375;
 DT 01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1997, sequence version 2.
 DT 07-MAR-2006, entry version 51.
 DE 6-phospho-beta-glucosidase ascb (EC 3.2.1.86).
 GN Name=ascB; OrderedLocustNames=b2716;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC STRAIN=K12;
 RX MEDLINE=92334140; PubMed=1630307;
 RA Hall B.G., Xu L.;
 RT "Nucleotide sequence, function, activation, and evolution of the
 RT cryptic asc operon of Escherichia coli K12.";
 RL Mol. Biol. Evol. 9:688-706(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- FUNCTION: Can hydrolyze salicin, cellobiose, and probably arbutin.
 CC -1- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucosyl-(1,4)-D-glucose +
 CC H(2)O = D-glucose + D-glucose 6-phosphate.
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 1 family.

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CC EMBL; M73326; AAA1430.1; -; Unassigned DNA.
 DR EMBL; U29579; AAA69226.1; ALT INIT; Genomic DNA.
 DR EMBL; U00096; AAC75758.1; -; Genomic DNA.
 DR FTR; H65051; H65051.
 DR HSP; P11546; 1PBG.
 DR GenomeReviews; U00096_GR; b2716.
 DR EcoBASE; EB0083; -;
 DR EcoGene; EG10085; ascb.
 DR BioCyc; EcoCyc:EG10085-MONOMER; -;
 DR InterPro; IPR001360; Glyco_hydro_1.
 DR PANTHER; PTHR10353; Glyco_hydro_1; 1.
 DR Pfam; PF00232; Glyco_hydro_1; 1.
 DR PRINTS; PR00131; GLYHYDRLASE1.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
 DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
 KM Complete proteome; Glycosidase; Hydrolase.
 FT CHAIN 1 474
 FT ACT_SITE 180 180
 FT ACT_SITE 372 372
 FT ACT_SITE 405 406
 FT CONFLICT 428 428
 FT CONFLICT 455 456
 FT CONFLICT 474 AA; 53935 MW; 02ACE6BBEP211011 CRC64;
 SQ SEQUENCE 474 AA; 53935 MW; 02ACE6BBEP211011 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 474;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
 |||||
 DB 157 FSRYAR 162

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RESULT 21
Q31X80_SHIDS PRELIMINARY; PRT; 474 AA.
ID Q31X80;
AC Q31X80;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE 6-phospho-beta-glucosidase, cryptic.
GN Name=ascB; OrderedlocusNames=SB02802;
OS Shigella boydii serotype 4 (strain Sb227).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300267;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=16275786; DOI=10.1093/nar/gki954;
RX Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).

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DR EMBL; CP000036; AB67328.1; -; Genomic DNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KM Complete proteome.
SQ SEQUENCE 474 AA; 53786 MW; 54823AE3832FF87F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 157 FSRYAR 162

RESULT 22
Q32CL4_SHIDS PRELIMINARY; PRT; 474 AA.
ID Q32CL4;
AC Q32CL4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE 6-phospho-beta-glucosidase.
GN Name=ascB; OrderedlocusNames=SDY 2912;
OS Shigella dysenteriae serotype 1 (strain Sd197).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300267;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=16275786; DOI=10.1093/nar/gki954;
RX Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).

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DR EMBL; CP000034; AB67294.1; -; Genomic DNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KM Complete proteome.

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SQ SEQUENCE 474 AA; 53786 MW; A6572D302DCABCC8 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 157 FSRYAR 162

RESULT 23
Q3YER8_SHIDS PRELIMINARY; PRT; 474 AA.
ID Q3YER8;
AC Q3YER8;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE 6-phospho-beta-glucosidase, cryptic.
GN Name=ascB; OrderedlocusNames=SSO_2860; ORFNames=SSO_2860;
OS Shigella sonnei (strain SSO46).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300269;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=16275786; DOI=10.1093/nar/gki954;
RX Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).

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DR EMBL; CP000038; AA289464.1; -; Genomic DNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLYHYDROLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KM Complete proteome.
SQ SEQUENCE 474 AA; 53830 MW; 2FC8B759849919C7 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 157 FSRYAR 162

RESULT 24
Q2MAB3_ECOLI PRELIMINARY; PRT; 474 AA.
ID Q2MAB3;
AC Q2MAB3;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Cryptic 6-phospho-beta-glucosidase.
GN Name=ascB;
OS Escherichia coli W3110.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=316407;

RN NUCLEOTIDE SEQUENCE.

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RC STRAIN=K-12;
RX MEDLINE=81053692; PubMed=6159575;
RA Smith D.R., Calvo J.M.;
RT "Nucleotide sequence of the E coli gene coding for dihydrofolate
RT reductase.";
RL Nucleic Acids Res. 8:2255-2274(1980).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Sekiguchi T., Ortega-Cesena J., Nosch Y., Ohashi S., Tsuda K.,
RA Kanaya S.;
RT "DNA and amino-acid sequences of 3-isopropylmalate dehydrogenase of
RT Bacillus coagulans. Comparison with the enzymes of Saccharomyces
RT cerevisiae and Thermus thermophilus.";
RL Biochim. Biophys. Acta 867:36-44(1986).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
RT "Nucleotide sequence and deletion analysis of the polB gene of
RT Escherichia coli.";
RL DNA Cell Biol. 9:613-635(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Smallshaw J.E., Kelln R.A.;
RT "Cloning, nucleotide sequence and expression of the Escherichia coli
RT K-12 pyrH gene encoding UMP kinase.";
RL Genetics (Life Sci. Adv.) 11:59-65(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,
RA Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;
RT "Highly accurate genome sequences of Escherichia coli K-12 strains
RT MG1655 and W3110.";
RL Mol. Syst. Biol. 0:0-0(2006).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX PubMed=16397293; DOI=10.1093/nar/gk1150;
RA Rallev M., Abe T., Arnaud M.B., Berlyn M.K., Blattner F.R.,
RA Chaudhuri R.R., Glaeser J.D., Horiuchi T., Keseler I.M., Koenig T.,
RA Mori H., Perna N.T., Plunkett G. III, Rudd K.E., Serres M.H.,
RA Thomas G.H., Thomson N.R., Wishart D., Wanner B.L.;
RT "Escherichia coli K-12: a cooperatively developed annotation snapshot-
RT -2005.";
RL Nucleic Acids Res. 34:1-9(2006).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97349980; PubMed=9205837; DOI=10.1093/dnares/4.2.91;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubdam S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97251358; PubMed=9097040; DOI=10.1093/dnares/3.6.379;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubdam S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97251357; PubMed=9097039; DOI=10.1093/dnares/3.6.363;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubdam S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97034878; PubMed=8940112; DOI=10.1074/jbc.271.49.31145;
RA Arn E.A., Abelson J.N.;
RT "The 2'-5' RNA ligase of Escherichia coli. Purification, cloning, and
RT genomic disruption.";
RL J. Biol. Chem. 271:31145-31153(1996).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=8905232; DOI=10.1093/dnares/3.3.137;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Horjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 2.4-4.1 min (110,917-193,643 bp) region.";
RL Nucleic Acids Res. 22:1637-1639(1994).
RN [13]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94240115; PubMed=8183897;
RA Janosi L., Shimizu I., Kaji A.;
RT "Ribosome recycling factor (ribosome releasing factor) is essential
RT for bacterial growth.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4249-4253(1994).
RN [14]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94124004; PubMed=7904973; DOI=10.1016/0378-1119(93)90470-N;
RA Allikmets R., Gerrard B.C., Court D., Dean W.C.;
RT "Cloning and organization of the abc and mdl genes of Escherichia
RT coli: relationship to eukaryotic multidrug resistance.";
RL Gene 136:231-236(1993).
RN [15]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94018640; PubMed=8412694;
RA van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.D.;
RT "The genes of the gluconate synthase adenyllylation cascade are not
RT regulated by nitrogen in Escherichia coli.";
RL Mol. Microbiol. 9:443-458(1993).
RN [16]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=93259920; PubMed=8387990;
RA Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;

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RT  "Rhs elements of Escherichia coli K-12: complex composites of shared
RT  and unique components that have different evolutionary histories.";
RL  J. Bacteriol. 175:2799-2808(1993).
RN  (17)
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=K-12;
RX  MEDLINE=93123180; PubMed=8419307;
RA  Yamada M., Asaoka S., Saiter M.H. Jr., Yamada Y.;
RT  "Characterization of the gsd gene from Escherichia coli K-12 W3110 and
RT  regulation of its expression.";
RL  J. Bacteriol. 175:568-571(1993).
RN  (18)
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=K-12;
RX  MEDLINE=93116053; PubMed=1474579;
RA  Cornack R.S., Mackie G.A.;
RT  "Structural requirements for the processing of Escherichia coli S S
RT  ribosomal RNA by RNase E in vitro.";
RL  J. Mol. Biol. 228:1078-1090(1992).
RN  (19)
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=K-12;
RX  MEDLINE=93094132; PubMed=1459951;
RA  Gervais F.G., Drapeau G.R.;
RT  "Identification, cloning, and characterization of rcsF, a new
RT  regulator gene for exopolysaccharide synthesis that suppresses the
RT  division mutation fts284 in Escherichia coli K-12.";
RL  J. Bacteriol. 174:8016-8022(1992).
RN  (20)
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=K-12;
RX  MEDLINE=93077430; PubMed=1447125;
RA  Yamataka K., Ogura T., Niki H., Hiraga S.;
RT  "Identification and characterization of the smbA gene, a suppressor of
RT  the mukB null mutant of Escherichia coli.";
RL  J. Bacteriol. 174:7517-7526(1992).
RN  (21)
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=K-12;
RX  MEDLINE=93011013; PubMed=1396599;
RA  Condon C., Phillips J., Fu Z.Y., Squires C., Squires C.L.;

Query Match      100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 FSRYAR 6
    |||||
Db  157 FSRYAR 162

RESULT 25
O8X841 EC057
AC O8X841 EC057 PRELIMINARY; PRT; 474 AA.
DT 01-MAR-2002. Integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE 6-phospho-beta-glucosidase; cryptic (6-phospho-beta-glucosidase).
GN Nameas8B; OrderedlocusNames=EC63572, z4024;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Berra N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.V., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimailanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

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RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN (2)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/nar/8.1.11;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
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CC -----
DR EMBL; AB005174; AAG57823.1; -; Genomic DNA.
DR EMBL; BA000007; BAB36995.1; -; Genomic DNA.
DR PIR; C85920; C85920.
DR PIR; D91075; D91075.
DR HSSP; P11546; IPBG.
DR BIOCyc; EC048334-1:EC53572-MONOMER; -.
DR GO; GO:0004553; F.hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P.carbohydrate metabolism, IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR PANTHER; PTHR10353; Glyco_hydro_1; 1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Complete proteome.
SQ SEQUENCE 474 AA; 53731 MW; 7B31E492C9ABD14 CRC64;

Query Match      100.0%; Score 31; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 FSRYAR 6
    |||||
Db  157 FSRYAR 162

RESULT 26
O3XAM6 PSEPP PRELIMINARY; PRT; 494 AA.
AC O3XAM6;
DT 08-NOV-2005. Integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 4.
DE Permease for cytosine/purines, uracil, thiamine, allantoin.
GN OrderedlocusNames=Pfl_3440;
OS Pseudomonas fluorescens (strain Pfo-1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205922;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Istrati S., Plunkett S., Saunders E.H., Schmutz J.,
RA Lartner F., Land M., Kyriakides N., Anderson I., Richardson P.;
RT "Complete sequence of Pseudomonas fluorescens Pfo-1.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000094; ABA75178.1; -; Genomic DNA.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0015205; F.nucleobase transporter activity; IEA.
DR GO; GO:0015931; P.nucleobase, nucleoside, nucleotide and nucl. . .; IEA.

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DR InterPro: IPR001248; Cyt_pur_permease.
DR Pfam: PF02133; Transp_cyt_pur; 1.
KW Complete proteome.
SQ SEQUENCE 494 AA; 53346 MW; 593C147D6A2D89FD CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 494;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 257 FSRYPAR 262

RESULT 27
Q2X8L3_PSEPU PRELIMINARY; PRT; 496 AA.
AC Q2X8L3_
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Transporter, NCS1 nucleoside transporter family.
GN ORFNames=PputDRAFT_0203;
OS Pseudomonas putida_F1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=351746;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=F1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Pseudomonas putida F1."
RT "Sequencing of the draft genome and assembly of Pseudomonas putida F1."
RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=F1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Pseudomonas putida F1."
RT Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
RT "CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data."
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CC -----
DR EMBL: AALM01000087; EAP48124.1; -; Genomic_DNA.
DR SQUENCE 496 AA; 53548 MW; 4681791B53DFB357 CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 496;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 257 FSRYPAR 262

RESULT 28
Q88FQ2_PSEPK PRELIMINARY; PRT; 496 AA.
AC Q88FQ2_
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Transporter, NCS1 nucleoside transporter family.
GN OrderedLocNames=PP4035; ORFNames=PP_4035;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beaman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfel E.K., Scanlan D., Tran K.,
RA Moazzes A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Medler H., Lauber J., Stegandic D., Hohnselt J., Straczek M., Helm S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
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CC -----
DR EMBL: AE015451; AAN69627.1; -; Genomic_DNA.
DR TIGR: PP4035;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0015205; F:nucleoside transporter activity; IEA.
DR GO: GO:0015931; P:nucleoside, nucleoside, nucleotide and nucl. .; IEA.
DR InterPro: IPR001248; Cyt_pur_permease.
DR Pfam: PF02133; Transp_cyt_pur; 1.
KW Complete proteome.
SQ SEQUENCE 496 AA; 53520 MW; 4681791B4CCFB357 CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 496;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYPAR 6
Db 257 FSRYPAR 262

RESULT 29
Q91674_PSEAE PRELIMINARY; PRT; 496 AA.
AC Q91674_
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Probable transporter.
GN OrderedLocNames=PA0443;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35020707;
RX Stover C.K., Pham X.-O.T., Erwin A.L., Mitsuuchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.U., Coulter S.N., Folger K.R., Kae A., Lapidis K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
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CC -----
DR EMBL: AE004481; AAG03832.1; -; Genomic_DNA.
DR F1R; B83591; B83591.

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DR BiOCCy: PAER287:PA0443-MONOMER: -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0015205; F:nucleobase transporter activity; IEA.
DR GO: GO:0015931; F:nucleobase, nucleoside, nucleotide and nucl. . .; IEA.
DR InterPro: IPR001248; Cyt pur permease.
DR Pfam: PF02133; Transp_cyt_pur; 1.
KM Complete proteome.
SQ SEQUENCE 496 AA; 53681 MW; C9DAC0428B2D4C7 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
DB 257 FSRYPAR 262

RESULT 30
ID Q3BYW8_XANCS PRELIMINARY; PRT; 526 AA.
AC Q3BYW8;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DE Gamma-glutamyltranspeptidase (EC 2.3.2.2).
GN Name-egg11; OrderedLocNames=XCV0314;
OS Xanthomonas campestris pv. vesicatoria (strain 85-10).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=316273;
RN 1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16237009; DOI=10.1126/JB.187.21.7254-7266.2005;
RA Thieme F., Koehnig R., Bekel T., Berger C., Boch J., Buettner D.,
RA Caldana C., Gaigalat U., Goemann A., Kay S., Kirchner O., Lanz C.,
RA Linke B., McHardy A.C., Meyer F., Mittenhuber G., Nies D.H.,
RA Niebach-Kloessen U., Patrschkowski T., Rueckert C., Rupp O.,
RA Schneider S., Schuster S.C., Vorhoeft F.J., Weber E., Puhler A.,
RA Bona U., Bartsels D., Kaiser O.;
RT "Insights into genome plasticity and pathogenicity of the plant
RT pathogenic bacterium Xanthomonas campestris pv. vesicatoria revealed
RT by the complete genome sequence.";
RL J. Bacteriol. 187:7254-7266(2005).
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CC -----
DR EMBL: AM039952; CAJ21945.1; -; Genomic DNA.
DR GO: GO:0008415; F:acyltransferase activity; IEA.
DR GO: GO:0003840; F:gamma-glutamyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
KM Acyltransferase; Complete proteome; Transferase.
SQ SEQUENCE 526 AA; 55499 MW; B40B3B743818AA43 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
DB 434 FSRYPAR 439

RESULT 31
ID Q8POL8_XANAC PRELIMINARY; PRT; 526 AA.
AC Q8POL8;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Gamma-glutamyltranspeptidase.
GN Name=gtc;

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OS Xanthomonas axonopodis pv. citri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN 1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Queglio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergro F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Melandis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spínola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitejima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
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CC -----
DR EMBL: AE011655; AAM35197.1; -; Genomic DNA.
DR MEROPS; T03_014; -.
DR LinkHub; Q8POL8; -.
DR GO: GO:0008440; F:gamma-glutamyltransferase activity; IEA.
DR InterPro: IPR001011; GGT_peptidase.
DR PANTHER: PTHR11686; GGT_peptidase; 1.
DR Pfam: PF01019; G_glu_transpept; 1.
DR PRINTS; PR01210; GGTTRANSPTASE.
DR TIGRFAMs; TIGR00066; g_glu_trans; 1.
KM Complete proteome.
SQ SEQUENCE 526 AA; 55544 MW; C841558896A9B64 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
DB 434 FSRYPAR 439

RESULT 32
ID Q7SA29_NEUCR PRELIMINARY; PRT; 560 AA.
AC Q7SA29;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN ORFNames=NCU07334.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN 1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Futrell S., Reiman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,

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RA Zelter A., Schultze U., Koche G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Strange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamysseilis M.,
RA Mancini E., Bielke C., Rudd S., Fishman D., Krystofova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catchside D.E.A., Li W., Pratt R.J., Osman S.A.,
RA Desouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Sella S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RT Nature 422:859-868(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AABX01000207; EAA33256.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015205; F:nucleobase transporter activity; IEA.
DR GO; GO:0015931; P:nucleobase, nucleoside, nucleotide and nucl. . .; IEA.
DR InterPro; IPR001248; Cyt_pur_permease.
DR InterPro; IPR012681; NCS1.
DR Pfam; PF02133; Transp_cyt_pur; 1.
DR TIGRFAMs; TIGR00800; ncs1; 1.
KM Hypothetical protein.
SQ SEQUENCE 560 AA; 62325 MW; FAC13B1A5F26565 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 269 FSRYAR 274

RESULT 33
Q21282_RHOA PRELIMINARY; PRT; 635 AA.
AC Q21282;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DE Extracellular solute-binding protein, family 5 precursor.
GN ORFNames=RPB_1770;
OS Rhodospseudomonas palustris Ha2.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodospseudomonas.
OX NCBI_TaxID=316058;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ha2;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pliuck S., Chain P., Malfacti S., Shin M.,
RA Verger L., Schmutz J., Larimer F., Land M., Hauser L., Pelletier D.A.,
RA Kyriades N., Anderson I., Oda Y., Harwood C.S., Richardson P.;
RT "Complete sequence of Rhodospseudomonas palustris Ha2.";
RT Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000250; ABD06478.1; -; Genomic_DNA.
KM Signal.
FT SIGNAL 1 36 Potential.
SQ SEQUENCE 635 AA; 71469 MW; 08D975473193E710 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 595 FSRYAR 600

RESULT 34
Q374J7_RHOA PRELIMINARY; PRT; 663 AA.
ID Q374J7_RHOA
AC Q374J7;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Twin-arginine translocation pathway signal precursor.
GN ORFNames=RPEDRAFT_2330;
OS Rhodospseudomonas palustris BisA53.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodospseudomonas.
OX NCBI_TaxID=316055;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BisA53;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pliuck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Rhodospseudomonas
RT palustris BisA53.";
RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BisA53;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome of Rhodospseudomonas palustris
RT BisA53." (OCT-2005) to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AALA01000008; EAO90388.1; -; Genomic_DNA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
KM Signal.
FT SIGNAL 663 663 Potential.
SQ SEQUENCE 663 AA; 74262 MW; 32F26A217EC705E4 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 622 FSRYAR 627

RESULT 35
Q4SCJ9_TETNG PRELIMINARY; PRT; 809 AA.
ID Q4SCJ9_TETNG
AC Q4SCJ9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Chromosome undetermined SCAP14653, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTEING0020461001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OK NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallion O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
 Mauceli E., Bonneau L., Fischer C., Orouf-Coataz C., Barrot A.,
 Nicard S., Jaffe D., Fisher S., Jutfalla G., Dossat C., Segurens B.,
 Dastiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 Biemont C., Skali Z., Catolico L., Poulain J., De Berardinis V.,
 Cruaud C., Duprat S., Brotier P., Coutanceau J.-P., Gonzy J.,
 Parra G., Lardier G., Chapple C., McKernan K.J., McMan P., Bosak S.,
 Kellis M., Wolf J.-N., Guigo R., Zody M.C., Mesirov J.,
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
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 CC -----
 DR EMBL: CAAB01014653; CAG01633.1; -, Genomic DNA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0006869; P:lipid transport; IEA.
 DR GO: GO:0008202; P:steroid metabolism; IEA.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR000648; Oxyterol_bd.
 DR InterPro: IPR001849; PH.
 DR PANTHER: PTHR10972; Oxyterol_BP; 1.
 DR Pfam: PF01237; Oxyterol_BP; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PROSITE: PS01013; OSBP; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR Lipid transport; Transport.
 KW NON TER 809 809
 SQ SEQUENCE 809 AA; 91216 MW; 3199F0A349871EB4 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 809;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 DB 742 FSRYAR 747

RA Birren B.W., Nusbaum C., Abebe A., Abouelell A., Adekoya E.,
 RA Alt-Zahra M., Allen R., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H.M., Amburster J., Bachantang P., Baldwin J., Barry A.,
 RA Bayut T., Blichstein B., Bloom T., Biye J., Boguslavsky L.,
 RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S.E., Camarata J., Campo K., Chang J., Cheshatsang Y.,
 RA Citeron M., Collamore A., Considine T., Cook A., Cooke P., Corum B.,
 RA Cuomo C., David R., Dawoe T., Degray S., Dodge S., Doolley K.,
 RA Dorje P., Dorje K., Doris L., Dufey N., Dupes A., Elkins T.,
 RA Engels R., Erickson J., Farina A., Fato S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley J., Gage D., Galegan J.B., Geatin G., Gierle S.,
 RA Ghitke A., Goyette A., Gajam J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husbey E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kanysseis M., Karlsson E.,
 RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
 RA Lui A., Ma L.-d., Mabbitt R., MacDonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., McGhee T., Meldrum J., Menes L.,
 RA Mesirov J., Minalev A., Minova T., Mikelsen T., Mlenga V., Noru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C.B., Nizzari M., Norbu C.,
 RA Norbu N., O'Donnell P., Okoawo O., O'Leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhuan P., Pigani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond B.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Rutman J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stealer J., Stange-Thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuina P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamir T., Tsono N., Vallee D., Vassiliou H.,
 RA Venkatasam V.S., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
 RA Zimmer A., Zody M., Lander E.S.,
 RT "The genome sequence of *Ustilago maydis*."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
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 CC -----
 DR EMBL: AACP01000149; EAK85206.1; -, Genomic DNA.
 DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO: GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO: GO:0006512; P:ubiquitin cycle; IEA.
 DR GO: GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro: IPR006035; Arg_agm_form.
 DR InterPro: IPR006615; Pept_C19_N1.
 DR InterPro: IPR001394; Peptidase_C19.
 DR Pfam: PF00443; UCH; 1.
 DR SMART: SM00695; DUSP; 1.
 DR PROSITE: PS00147; ARGINASE_1; UNKNOWN_1.
 DR PROSITE: PS00972; UCH_2_1; 1.
 DR PROSITE: PS00973; UCH_2_2; 1.
 DR PROSITE: PS50235; UCH_2_3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1427 AA; 156945 MW; BBB060C165811664 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 1427;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 DB 896 FSRYAR 901

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RESULT 37
Q57UM9_9TRYRP PRELIMINARY; PRT; 1649 AA.
AC Q57UM9_9
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DE 07-FEB-2006, entry version 1.
GN Mitochondrial DNA polymerase I protein C.
OS Trypanosoma brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
  Johnson J., Jones K., Koo H.L., Larkin C., Pal G., Peterson J.,
  Ralalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
  Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
  Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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EMBL; AC159450; AAX70690.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR001098; DNA_pol.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00868; DNAPOLI.
DR PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN 1.
SQ SEQUENCE 1649 AA; 182029 MW; 2FC69472CC2A1A1E CRC64;

Query Match 100.0%; Score 31; DB 2; Length 1649;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYP 6
Db 5 FSRYP 10

RESULT 38
Q8MWB3_9TRYRP PRELIMINARY; PRT; 1649 AA.
AC Q8MWB3_9
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DE 07-FEB-2006, entry version 1.
DE DNA polymerase I-like protein C.
GN Name=POLIC;
OS Trypanosoma brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TREU927;
RA Klingbeil M.M., Motyka S.A., Englund P.T.;
  Multiple mitochondrial DNA polymerases in Trypanosoma brucei.;
  Mol. Cell 10:1175-186(2002).
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EMBL; AF445378; AAM81964.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR001098; DNA_pol.

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DR InterPro; IPR002298; DNA_polI.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00868; DNAPOLI.
DR PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN 1.
SQ SEQUENCE 1649 AA; 182043 MW; 2DAABC3C7373BB0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 1649;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYP 6
Db 5 FSRYP 10

RESULT 39
Q49100_MYCCA PRELIMINARY; PRT; 37 AA.
AC Q49100_1
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DE 07-FEB-2006, entry version 1.
DE DNA gyrase subunit A (Fragment).
GN Name=gyrA;
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC27343;
RX MEDLINE=95129856; PubMed=7828871; DOI=10.1016/0378-1119(94)90653-X;
RA Sano K., Miyata M.;
  "The gyrB gene lies opposite from the replication origin on the
  RT circular chromosome of Mycoplasma capricolum.";
  Gene 151:181-183(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC27343;
RA Sano K., Miyata M.;
  Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC27343;
RA Sano K.-I.;
  Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
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EMBL; D26016; BAA05032.1; -; Genomic_DNA.
DR NON TER 37
FT SEQUENCE 37 AA; 4428 MW; 0C83911EFCE84697 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 37;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYP 6
Db 20 FSRYP 25

RESULT 40
Q56EC7_9CAUD PRELIMINARY; PRT; 102 AA.
AC Q56EC7_9
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DE 07-FEB-2006, entry version 1.
DE Hypothetical protein PHG310R237C.
GN Name=PHG310R237C; ORFNames=PHG31p234;
OS Aeromonas phage 31.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.

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OX NCBI_TaxID=321023;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nolan J.M., Petrov V., Bertrand C., Kirsch H.M., Karam J.D.;
 RT "Comparative analysis of the Aeromonas bacteriophage 31 genome."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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 CC EMBL: AY962392; AA63723.1; -; Genomic_DNA.
 DR Hypochemical protein.
 KM SEQUENCE 102 AA; 11960 MW; B591B2BF81A9A58E CRC64;
 SQ
 Query Match 90.3%; Score 28; DB 2; Length 102;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSRYAR 6
 Db 68 FNRYYAR 73
 RESULT 41
 OSU3N8 BRABE
 ID Q5U3N8 PRELIMINARY; PRT; 110 AA.
 AC Q5U3N8;
 DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Hypochemical protein.
 GN Name=wrB;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Larvae;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toibiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schenarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Larvae;
 RA Director MGC Project;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC085456; AA85456.1; -; mRNA.
 DR Ensemble; ENSDARG0000024641; Danio rerio.
 ZFIN: ZDB-GENE-030131-7696; wrB.

DR InterPro: IPR007514; CHD5.
 DR Pfam: PF04420; CHD5. 1.
 KM Hypochemical protein.
 SQ SEQUENCE 110 AA; 12330 MW; 2496B215D029C793 CRC64;
 QY 1 FSRYAR 6
 Db 5 FARYAR 10
 RESULT 42
 Q5ZJM2 CHICK
 ID Q5ZJM2 CHICK PRELIMINARY; PRT; 126 AA.
 AC Q5ZJM2;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypochemical protein.
 GN ORFNames=RCJMB04.17c17;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
 RA Friedler P., Kutter S., Biagodatki A., Kostovska D., Kocer M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
 RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
 RT gene function analysis";
 RL Genome Biol. 6:R6-R6(2005).
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 CC -----
 CC EMBL: AJ720412; CAG32071.1; -; mRNA.
 DR InterPro: IPR007514; CHD5.
 DR Pfam: PF04420; CHD5. 1.
 KM Hypochemical protein.
 SQ SEQUENCE 126 AA; 14426 MW; 30A1186080FEB32B CRC64;
 QY 1 FSRYAR 6
 Db 21 FARYAR 26
 RESULT 43
 Q3J0B8 BURP1
 ID Q3J0B8 BURP1 PRELIMINARY; PRT; 133 AA.
 AC Q3J0B8;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 21-FEB-2006, entry version 4.
 DE Hypochemical protein.
 GN OrderedLocNames=BURPS1710b_2850;
 OS Burkholderia pseudomallei (strain 1710b).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 OX NCBI_TaxID=320372;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Woods D.E., Nieman W.C.;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.

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CC -----
DR EMBL: CP000124; AB48582.1; -, Genomic_DNA.
DR TIGR: B0RPS1710D.2850; -.
DR InterPro: IPR011633; DUF1602.
DR Pfam: PF07673; DUF1602; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 133 AA; 14144 MW; C069DFC776D45162 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 133;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 80 FSRYSR 85

RESULT 44
ID Q52KS6_XENLA PRELIMINARY; PRT; 170 AA.
AC Q52KS6;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
NC NCB1_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguélano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC094207; AA94207.1; -, mRNA.
DR Hypothetical protein.
KM Hypothetical protein.
SQ SEQUENCE 170 AA; 19413 MW; 0E07DAB1E23F6A4A CRC64;

Query Match          90.3%; Score 28; DB 2; Length 170;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 65 FARYAR 70

RESULT 45
ID Q6DRM0_BRARE PRELIMINARY; PRT; 170 AA.
AC Q6DRM0;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Pindall wizard.
DE Name=wrdb;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NC NCB1_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RT development";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
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CC -----
DR EMBL: AY648739; AAT68057.1; -, mRNA.
DR Ensembl: ENSDARG0000024641; Danio rerio.
DR ZFIN: ZDB-GENE-030131-7696; wrdb.
DR InterPro: IPR007514; CHDS.
DR Pfam: PF04420; CHDS; 1.
SQ SEQUENCE 170 AA; 19219 MW; 4F4350EB2C29184E CRC64;

Query Match          90.3%; Score 28; DB 2; Length 170;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 65 FARYAR 70

RESULT 46
ID Q5AAR5_CANAL PRELIMINARY; PRT; 171 AA.
AC Q5AAR5;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
DE ORFNames=CaO19.7533;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
NC NCB1_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RL STRAIN=SC5314;
RC -----
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RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Daves B.B., Newport G., Thorstenson Y.R., Agabidian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL, AAC001000039; EAK99775.1; -; Genomic_DNA.
DR Hypothetical protein.
SQ SEQUENCE 171 AA; 17791 MW; 032B4864D7C8B2E CRC64;

Query Match
Best Local Similarity 83.3%; Score 28; DB 2; Length 171;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
DB 24 FSRYSR 29

RESULT 47
WRB_HUMAN STANDARD; PRT; 174 AA.
ID WRB_HUMAN
AC 000258; O60740;
DT 01-NOV-1997; Integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000; sequence version 2.
DT 07-FEB-2006; entry version 34.
DE Trypophan-rich protein (Congenital heart disease 5 protein).
GN Name=WRB; Synonyms=CHD5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND SUBCELLULAR LOCATION.
RC TISSUE=Heart;
RX MEDLINE=98204400; PubMed=9544840; DOI=10.1007/s004330050693;
RA Egea A., Mazocco M., Sotgia F., Arrigo P., Oliva R., Bergonzi S.,
RA Nizetic D., Rasore-Quartino A., Scartezini P.;
RT "Identification and characterization of a new human cDNA from
RT chromosome 21q22.3 encoding a basic nuclear protein.";
RL Hum. Genet. 102:289-293(1998).

[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Tautien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
RA Rosenblatt A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Matsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordstiek G., Hornisch K., Brandt P.,
RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
RA Ramer J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrich H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).

[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.V., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Nucleus.
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CC -----
DR EMBL, Y12478; CAA73081.1; -; mRNA.
DR EMBL, AF064861; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL, AL163279; CAB90454.1; -; Genomic_DNA.
DR EMBL, BC012415; AAH12415.1; -; mRNA.
DR Ensembl, ENSG00000182093; Homo sapiens.
DR H-InvDB, HIX0016117; -.
DR HGNC, HGNC:12790; WRB.
DR MIM, 602915; Gene.
DR GO, GO:0005634; C:nucleus; TAS.
DR InterPro, IPR007514; CHD5.
DR Pfam, PF04420; CHD5; 1.
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FT CHAIN 1 174
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DB 69 FARYAR 74

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AC O8K0D7; O9D1W0;
DT 10-MAY-2005; Integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002; sequence version 1.
DT 07-FEB-2006; entry version 18.
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RA Davis M.J., Wilming L.G., Aldins V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
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RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
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RA Guatrich S., Harbers M., Hayaishi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Ikama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kumerfeldt S.K.,
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RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motegut-Tajer S., Mulder N., Nakano N., Nakauchi H., Ng P.,
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RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
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RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Ikeda J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Maki K., Matabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayaishi Y.,
RT "The transcriptional landscape of the mammalian genome.",
RL Science 309:1559-1563(2005).
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RA Brownstein M.J., Uscin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Feby J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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DT 21-DEC-2004, sequence version 1.
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DT 10-MAY-2005, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
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CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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GenCore version 5.1.9
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OM protein - protein search, using sw model

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50.808 Million cell updates/sec

Title: US-10-541-343-2

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117	25	80.6	658	1	US-08-190-802A-34	Sequence 34, Appl	190	24	77.4	501	2	US-09-270-767-4373	Sequence 4373, A
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119	25	80.6	658	2	US-08-473-089-34	Sequence 34, Appl	192	24	77.4	512	2	US-09-716-865-14	Sequence 14, Appl
120	25	80.6	658	2	US-08-487-072A-34	Sequence 34, Appl	193	24	77.4	523	2	US-09-538-092-571	Sequence 571, App
121	25	80.6	822	2	US-09-826-312A-12	Sequence 12, Appl	194	24	77.4	530	2	US-09-270-767-46567	Sequence 46567, A
122	25	80.6	822	2	US-09-542-497A-12	Sequence 12, Appl	195	24	77.4	531	2	US-09-489-039A-9781	Sequence 9781, Ap
123	25	80.6	822	2	US-10-108-767-12	Sequence 12, Appl	196	24	77.4	536	2	US-09-252-991A-20771	Sequence 20771, A
124	25	80.6	822	2	US-10-152-156-12	Sequence 12, Appl	197	24	77.4	560	2	US-09-489-039A-11940	Sequence 11940, A
125	25	80.6	822	3	US-10-835-096-12	Sequence 12, Appl	198	24	77.4	563	2	US-09-437-568A-21	Sequence 21, Appl
126	25	80.6	850	2	US-09-893-525-42	Sequence 42, Appl	199	24	77.4	575	2	US-09-252-991A-26328	Sequence 26328, A
127	25	80.6	921	2	US-09-543-681A-5734	Sequence 5734, Ap	200	24	77.4	587	2	US-09-902-540-15496	Sequence 15496, A
128	25	80.6	925	1	US-08-252-995D-4	Sequence 4, Appl1	201	24	77.4	719	2	US-09-252-991A-22278	Sequence 22278, A
129	25	80.6	925	1	US-08-834-108-4	Sequence 4, Appl1	202	24	77.4	732	2	US-10-070-634-6	Sequence 6, Appl1
130	25	80.6	943	2	US-10-104-047-2552	Sequence 2552, Ap	203	24	77.4	1142	2	US-09-252-991A-18234	Sequence 18234, A
131	25	80.6	1077	2	US-09-949-016-11650	Sequence 11650, A	204	24	77.4	1456	1	US-08-803-973-2	Sequence 2, Appl1
132	25	80.6	1427	2	US-09-538-092-1044	Sequence 1044, Ap	205	24	77.4	1456	1	US-08-803-972-2	Sequence 2, Appl1
133	25	80.6	2628	2	US-09-413-814-11	Sequence 11, Appl	206	24	77.4	1968	1	US-07-745-206A-7	Sequence 7, Appl1
134	25	80.6	2802	2	US-09-542-331-1	Sequence 1, Appl1	207	24	77.4	1968	1	US-08-455-543A-45	Sequence 45, Appl
135	25	80.6	2802	2	US-09-510-731-1	Sequence 1, Appl1	208	24	77.4	1968	1	US-08-223-305C-45	Sequence 45, Appl
136	24	77.4	14	1	US-08-465-325-16	Sequence 126, App	209	24	77.4	1968	1	US-08-311-363-7	Sequence 7, Appl1
137	24	77.4	95	2	US-09-115-737-126	Sequence 126, App	210	24	77.4	10	2	US-08-159-339A-296	Sequence 296, App
138	24	77.4	101	2	US-09-252-991A-25355	Sequence 25355, A	211	23	74.2	11	2	US-08-403-459-37	Sequence 37, Appl
139	24	77.4	107	2	US-09-134-001C-636	Sequence 636, Ap	212	23	74.2	13	2	US-08-403-459-40	Sequence 40, Appl
140	24	77.4	136	2	US-09-248-796A-26186	Sequence 26186, A	213	23	74.2	14	1	US-08-467-083-64	Sequence 64, Appl
141	24	77.4	162	2	US-09-489-039A-8896	Sequence 8896, Ap	214	23	74.2	14	1	US-08-414-417B-64	Sequence 64, Appl
142	24	77.4	186	2	US-09-732-210-43	Sequence 43, Appl	215	23	74.2	14	1	US-08-466-348A-64	Sequence 64, Appl
143	24	77.4	215	2	US-09-489-039A-9863	Sequence 9863, Ap	216	23	74.2	14	1	US-08-468-545B-64	Sequence 64, Appl
144	24	77.4	215	2	US-09-252-991A-17696	Sequence 17696, A	217	23	74.2	14	2	US-08-466-680B-64	Sequence 64, Appl
145	24	77.4	249	2	US-09-252-991A-10185	Sequence 30185, A	218	23	74.2	14	2	US-09-027-998A-11	Sequence 11, Appl
146	24	77.4	283	2	US-09-583-110-4252	Sequence 4252, Ap	219	23	74.2	14	2	US-08-403-459-38	Sequence 38, Appl
147	24	77.4	286	2	US-09-107-532A-6850	Sequence 6850, Ap	220	23	74.2	14	2	US-08-403-459-39	Sequence 39, Appl
148	24	77.4	287	2	US-09-710-279-2538	Sequence 2538, Ap	221	23	74.2	14	2	US-08-403-459-45	Sequence 45, Appl
149	24	77.4	291	2	US-09-489-039A-7281	Sequence 7281, Ap	222	23	74.2	14	2	US-08-403-459-66	Sequence 66, Appl
150	24	77.4	302	2	US-09-270-767-59138	Sequence 59138, A	223	23	74.2	14	2	US-09-354-533-64	Sequence 64, Appl
151	24	77.4	307	2	US-09-489-039A-9062	Sequence 9062, Ap	224	23	74.2	14	2	US-09-943-692-11	Sequence 11, Appl
152	24	77.4	324	2	US-09-107-532A-6123	Sequence 6123, Ap	225	23	74.2	15	1	US-08-467-083-65	Sequence 50, Appl
153	24	77.4	331	1	US-08-180-209B-55	Sequence 55, Appl	226	23	74.2	15	1	US-08-414-417B-50	Sequence 50, Appl
154	24	77.4	331	1	US-08-180-209B-57	Sequence 57, Appl1	227	23	74.2	15	1	US-08-468-545B-50	Sequence 50, Appl
155	24	77.4	331	1	US-09-008-962-5	Sequence 5, Appl1	228	23	74.2	15	1	US-08-468-545B-50	Sequence 50, Appl
156	24	77.4	331	1	US-08-675-507-5	Sequence 5, Appl1	229	23	74.2	15	2	US-08-466-680B-50	Sequence 50, Appl
157	24	77.4	331	2	US-09-213-205-5	Sequence 5, Appl1	230	23	74.2	15	2	US-09-354-533-50	Sequence 50, Appl
158	24	77.4	331	2	US-08-474-883-55	Sequence 55, Appl	231	23	74.2	16	2	US-09-027-998A-20	Sequence 20, Appl
159	24	77.4	331	2	US-08-474-883-57	Sequence 57, Appl	232	23	74.2	16	2	US-09-943-692-20	Sequence 20, Appl
160	24	77.4	331	2	US-09-166-205B-55	Sequence 55, Appl	233	23	74.2	17	2	US-08-197-464-11	Sequence 11, Appl
161	24	77.4	331	2	US-09-166-205B-57	Sequence 57, Appl	234	23	74.2	17	5	PCT-US95-02121-11	Sequence 11, Appl
162	24	77.4	331	2	US-09-166-205B-70	Sequence 70, Appl	235	23	74.2	27	1	US-08-776-815B-14	Sequence 14, Appl
163	24	77.4	331	2	US-09-806-658-11	Sequence 11, Appl	236	23	74.2	27	1	US-08-776-815B-15	Sequence 15, Appl
164	24	77.4	331	2	US-09-806-658-12	Sequence 12, Appl	237	23	74.2	27	1	US-08-776-815B-15	Sequence 15, Appl
165	24	77.4	331	2	US-09-902-540-16733	Sequence 16733, A	238	23	74.2	27	2	US-08-737-629-3	Sequence 3, Appl
166	24	77.4	331	5	PCT-US94-02629-55	Sequence 55, Appl	239	23	74.2	28	1	US-08-776-815B-2	Sequence 2, Appl1
167	24	77.4	333	5	PCT-US94-02629-57	Sequence 57, Appl	240	23	74.2	29	1	US-08-776-815B-3	Sequence 3, Appl1
168	24	77.4	333	2	US-09-583-110-4033	Sequence 4033, Ap	241	23	74.2	29	1	US-08-776-815B-4	Sequence 4, Appl1
169	24	77.4	334	2	US-09-107-433-3718	Sequence 3718, Ap	242	23	74.2	30	1	US-08-776-815B-5	Sequence 5, Appl1
170	24	77.4	350	2	US-09-248-796A-18438	Sequence 18438, A	243	23	74.2	30	1	US-08-776-815B-6	Sequence 6, Appl1
171	24	77.4	355	2	US-09-248-796A-20711	Sequence 20711, A	244	23	74.2	30	1	US-08-776-815B-7	Sequence 7, Appl1
172	24	77.4	360	2	US-09-252-991A-31993	Sequence 31993, A	245	23	74.2	30	2	US-09-270-767-45041	Sequence 45041, A

245	23	74.2	30	2	US-09-270-767-60533	Sequence 60533, A	319	23	74.2	259	2	US-09-270-767-46318	Sequence 46318, A
247	23	74.2	30	2	US-09-623-548A-1300	Sequence 1300, Ap	320	23	74.2	251	7	5320958-5	Patent No. 5320958
248	23	74.2	30	2	US-09-657-276-1300	Sequence 1300, Ap	321	23	74.2	255	1	US-07-857-224B-66	Sequence 66, Appl
249	23	74.2	39	2	US-09-270-767-38754	Sequence 38754, A	322	23	74.2	257	1	US-09-489-039A-11725	Sequence 11725, A
250	23	74.2	39	2	US-09-270-767-53971	Sequence 53971, A	323	23	74.2	270	2	US-09-724-623-73	Sequence 73, Appl
251	23	74.2	45	1	US-08-056-200-98	Sequence 98, Appl	324	23	74.2	270	2	US-09-634-238-269	Sequence 269, App
252	23	74.2	45	1	US-08-800-644-98	Sequence 98, Appl	325	23	74.2	270	2	US-09-634-238-418	Sequence 418, Appl
253	23	74.2	47	1	US-08-625-322-22	Sequence 22, Appl	326	23	74.2	270	3	US-10-288-930-73	Sequence 73, Appl
254	23	74.2	47	1	US-08-625-322-23	Sequence 23, Appl	327	23	74.2	255	2	US-09-830-230A-217	Sequence 217, App
255	23	74.2	48	1	US-08-625-322-25	Sequence 25, Appl	328	23	74.2	259	2	US-09-184-658-63	Sequence 63, Appl
256	23	74.2	65	2	US-09-134-001C-2857	Sequence 2857, Ap	329	23	74.2	256	2	US-09-504-628-63	Sequence 63, Appl
257	23	74.2	67	2	US-09-248-796A-23905	Sequence 23905, A	330	23	74.2	262	2	US-09-515-806-19	Sequence 75, Appl
258	23	74.2	68	2	US-09-270-767-15068	Sequence 35068, A	331	23	74.2	302	2	US-09-599-806-75	Sequence 75, Appl
259	23	74.2	68	2	US-09-270-767-50285	Sequence 50285, A	332	23	74.2	304	2	US-09-543-681A-8069	Sequence 8069, Ap
260	23	74.2	74	7	5320958-12	Patent No. 5320958	333	23	74.2	308	2	US-09-252-991A-31739	Sequence 31739, A
261	23	74.2	82	1	US-09-513-999C-5490	Sequence 5490, Ap	334	23	74.2	311	2	US-09-248-796A-20384	Sequence 20384, A
262	23	74.2	82	1	US-07-881-075-19	Sequence 19, Appl	335	23	74.2	312	2	US-09-107-532A-6219	Sequence 6219, Ap
263	23	74.2	82	1	US-08-120-827-19	Sequence 19, Appl	336	23	74.2	314	2	US-09-270-767-38524	Sequence 38524, A
264	23	74.2	82	1	US-08-478-675-19	Sequence 19, Appl	337	23	74.2	314	2	US-09-270-767-53741	Sequence 53741, A
265	23	74.2	92	2	US-09-328-352-5171	Sequence 5171, Ap	338	23	74.2	315	2	US-09-958-969-2	Sequence 2, Appl
266	23	74.2	92	2	US-09-489-039A-13903	Sequence 13903, A	339	23	74.2	320	2	US-09-543-681A-6978	Sequence 6978, Ap
267	23	74.2	92	2	US-09-270-767-58919	Sequence 58919, A	340	23	74.2	327	2	US-09-252-991A-28744	Sequence 28744, A
268	23	74.2	94	1	US-08-467-822-38	Sequence 38, Appl	341	23	74.2	339	2	US-09-489-039A-8390	Sequence 8390, Ap
269	23	74.2	94	2	US-08-432-697-38	Sequence 38, Appl	342	23	74.2	331	2	US-08-778-717-21	Sequence 21, Appl
270	23	74.2	94	2	US-08-466-248-38	Sequence 38, Appl	343	23	74.2	331	2	US-09-710-279-3256	Sequence 3256, Ap
271	23	74.2	95	2	US-09-919-172-102	Sequence 102, App	344	23	74.2	340	2	US-09-540-236-2966	Sequence 2966, Ap
272	23	74.2	95	2	US-09-976-594-667	Sequence 467, App	345	23	74.2	342	1	US-08-454-196-2	Sequence 2, Appl
273	23	74.2	96	2	US-09-902-540-10579	Sequence 10579, A	346	23	74.2	342	2	US-09-064-033-2	Sequence 2, Appl
274	23	74.2	102	2	US-09-949-016-10557	Sequence 10557, A	347	23	74.2	342	2	US-09-291-046-2	Sequence 2, Appl
275	23	74.2	107	2	US-09-513-999C-5491	Sequence 5491, Ap	348	23	74.2	343	1	US-08-454-196-6	Sequence 6, Appl
276	23	74.2	114	2	US-09-252-991A-17800	Sequence 17800, A	349	23	74.2	343	1	US-08-286-819A-4	Sequence 4, Appl
277	23	74.2	116	2	US-09-184-658-48	Sequence 48, Appl	350	23	74.2	343	2	US-08-980-357-4	Sequence 4, Appl
278	23	74.2	116	2	US-09-504-262D-48	Sequence 48, Appl	351	23	74.2	343	2	US-09-064-033-6	Sequence 6, Appl
279	23	74.2	117	2	US-09-902-540-15284	Sequence 15284, A	352	23	74.2	343	2	US-09-291-046-6	Sequence 6, Appl
280	23	74.2	120	1	US-08-497-312-26	Sequence 26, Appl	353	23	74.2	343	2	US-09-357-735-4	Sequence 4, Appl
281	23	74.2	137	2	US-09-902-540-14040	Sequence 14040, A	354	23	74.2	348	2	US-09-107-532A-5305	Sequence 5305, Ap
282	23	74.2	137	2	US-09-270-767-32892	Sequence 32892, A	355	23	74.2	353	2	US-09-328-352-6721	Sequence 6721, Ap
283	23	74.2	138	2	US-09-270-767-48109	Sequence 48109, A	356	23	74.2	358	2	US-10-166-225A-109	Sequence 109, App
284	23	74.2	142	1	US-08-619-598-1	Sequence 1, Appl	357	23	74.2	359	1	US-07-881-075-2	Sequence 2, Appl
285	23	74.2	148	2	US-09-107-532A-3921	Sequence 3921, Ap	358	23	74.2	359	1	US-08-120-827-2	Sequence 2, Appl
286	23	74.2	150	2	US-09-252-991A-24718	Sequence 24718, A	359	23	74.2	360	2	US-08-478-675-2	Sequence 2, Appl
287	23	74.2	156	2	US-09-387-286-19	Sequence 19, Appl	360	23	74.2	360	2	US-09-252-991A-25388	Sequence 25388, A
288	23	74.2	160	2	US-09-957-641A-19	Sequence 19, Appl	361	23	74.2	360	2	US-09-710-279-2150	Sequence 2150, Ap
289	23	74.2	161	2	US-09-270-767-43460	Sequence 43460, A	362	23	74.2	365	2	US-09-949-016-7637	Sequence 7637, Ap
290	23	74.2	162	2	US-09-387-286-18	Sequence 18, Appl	363	23	74.2	366	2	US-09-543-681A-4553	Sequence 4553, Ap
291	23	74.2	162	2	US-09-270-767-46444	Sequence 46444, A	364	23	74.2	367	2	US-09-949-016-9429	Sequence 9429, Ap
292	23	74.2	167	2	US-10-104-047-3129	Sequence 3129, Ap	365	23	74.2	370	2	US-09-134-001C-3678	Sequence 3678, A
293	23	74.2	167	2	US-09-270-767-61958	Sequence 61958, A	366	23	74.2	371	2	US-10-081-644-2	Sequence 2, Appl
294	23	74.2	178	2	US-09-902-540-14484	Sequence 14484, A	367	23	74.2	371	2	US-09-270-767-43550	Sequence 43550, A
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296	23	74.2	188	2	US-09-252-991A-17818	Sequence 17818, A	369	23	74.2	376	1	US-07-881-075-51	Sequence 51, Appl
297	23	74.2	190	2	US-09-538-092-954	Sequence 954, App	370	23	74.2	380	1	US-08-120-827-51	Sequence 51, Appl
298	23	74.2	195	2	US-09-270-767-45424	Sequence 45424, A	371	23	74.2	380	1	US-08-478-675-51	Sequence 51, Appl
299	23	74.2	202	2	US-09-252-991A-25553	Sequence 25553, A	372	23	74.2	381	2	US-09-538-092-1017	Sequence 1017, Ap
300	23	74.2	205	2	US-09-724-797-50	Sequence 50, Appl	373	23	74.2	381	2	US-10-104-047-3169	Sequence 3169, Ap
301	23	74.2	210	2	US-09-171-461-34	Sequence 34, Appl	374	23	74.2	384	2	US-09-134-001C-5242	Sequence 5242, Ap
302	23	74.2	215	1	US-08-312-870-5	Sequence 5, Appl	375	23	74.2	385	5	FCT-US93-08528-31	Sequence 31, Appl
303	23	74.2	215	1	US-09-970-711-34	Sequence 34, Appl	376	23	74.2	385	5	US-08-118-270-31	Sequence 31, Appl
304	23	74.2	217	2	US-09-540-540-12408	Sequence 12408, A	377	23	74.2	385	5	US-09-252-991A-24433	Sequence 24433, A
305	23	74.2	221	2	US-08-778-717-4	Sequence 4, Appl	378	23	74.2	395	2	US-09-248-796A-16028	Sequence 16028, A
306	23	74.2	221	2	US-08-778-717-4	Sequence 4, Appl	379	23	74.2	398	1	US-08-630-822A-56	Sequence 56, Appl
307	23	74.2	228	2	US-09-489-039A-11967	Sequence 11967, A	380	23	74.2	398	1	US-09-005-069-56	Sequence 56, Appl
308	23	74.2	234	2	US-09-248-796A-20570	Sequence 20570, A	381	23	74.2	400	2	US-09-248-796A-23650	Sequence 23650, A
309	23	74.2	235	2	US-09-538-092-464	Sequence 464, App	382	23	74.2	402	2	US-09-489-039A-10525	Sequence 10525, A
310	23	74.2	243	2	US-09-902-540-15610	Sequence 15610, A	383	23	74.2	402	2	US-09-902-540-16610	Sequence 16610, A
311	23	74.2	244	2	US-09-710-279-994	Sequence 994, App	384	23	74.2	404	2	US-09-252-991A-8105	Sequence 8105, Ap
312	23	74.2	253	2	US-09-830-230A-218	Sequence 218, App	385	23	74.2	410	2	US-09-107-433-3915	Sequence 3915, Ap
313	23	74.2	254	2	US-09-247-373B-38	Sequence 38, Appl	386	23	74.2	415	2	US-09-554-999-2	Sequence 2, Appl
314	23	74.2	254	2	US-09-949-016-10670	Sequence 10670, A	387	23	74.2	415	2	US-10-188-586A-2	Sequence 2, Appl
315	23	74.2	257	2	US-09-489-039A-7196	Sequence 7196, Ap	388	23	74.2	415	2	US-09-758-759-145	Sequence 145, App
316	23	74.2	259	2	US-09-633-947B-3	Sequence 3, Appl	389	23	74.2	422	2	US-09-949-016-9757	Sequence 9757, Ap
317	23	74.2	259	2	US-09-543-681A-7362	Sequence 7362, Ap	390	23	74.2	422	2	US-09-270-767-46381	Sequence 46381, A
318	23	74.2	259	2			391	23	74.2	423	2		

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395	23	74.2	435	2	US-09-902-540-1518	Sequence 1518, A
396	23	74.2	436	2	US-09-252-991A-33064	Sequence 33064, A
397	23	74.2	444	2	US-09-252-991A-31017	Sequence 31017, A
398	23	74.2	446	1	US-08-307-444A-5	Sequence 5, Appli
399	23	74.2	446	1	US-08-307-389-5	Sequence 5, Appli
400	23	74.2	447	2	US-09-252-991A-28081	Sequence 28081, A
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404	23	74.2	453	1	US-08-767-993-11	Sequence 11, Appli
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407	23	74.2	456	1	US-08-587-389-3	Sequence 3, Appli
408	23	74.2	456	1	US-08-587-389-4	Sequence 4, Appli
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410	23	74.2	459	2	US-09-526-309B-3	Sequence 3, Appli
411	23	74.2	459	2	US-09-526-309B-5	Sequence 5, Appli
412	23	74.2	459	2	US-09-526-309B-7	Sequence 7, Appli
413	23	74.2	459	2	US-09-526-309B-9	Sequence 9, Appli
414	23	74.2	459	2	US-09-526-309B-11	Sequence 11, Appli
415	23	74.2	459	2	US-09-526-309B-13	Sequence 13, Appli
416	23	74.2	459	2	US-09-526-309B-17	Sequence 17, Appli
417	23	74.2	459	2	US-09-526-309B-19	Sequence 19, Appli
418	23	74.2	459	2	US-09-526-309B-21	Sequence 21, Appli
419	23	74.2	459	2	US-09-526-309B-23	Sequence 23, Appli
420	23	74.2	459	2	US-09-526-309B-25	Sequence 25, Appli
421	23	74.2	459	2	US-09-526-309B-27	Sequence 27, Appli
422	23	74.2	459	2	US-09-526-309B-29	Sequence 29, Appli
423	23	74.2	459	2	US-09-526-309B-31	Sequence 31, Appli
424	23	74.2	459	2	US-09-526-309B-33	Sequence 33, Appli
425	23	74.2	459	2	US-09-526-309B-35	Sequence 35, Appli
426	23	74.2	459	2	US-09-526-309B-37	Sequence 37, Appli
427	23	74.2	459	2	US-09-526-309B-39	Sequence 39, Appli
428	23	74.2	459	2	US-09-526-309B-41	Sequence 41, Appli
429	23	74.2	459	2	US-09-526-309B-43	Sequence 43, Appli
430	23	74.2	459	2	US-10-280-858A-1	Sequence 1, Appli
431	23	74.2	459	2	US-10-280-858A-3	Sequence 3, Appli
432	23	74.2	459	2	US-10-280-858A-5	Sequence 5, Appli
433	23	74.2	459	2	US-10-280-858A-7	Sequence 7, Appli
434	23	74.2	459	2	US-10-280-858A-9	Sequence 9, Appli
435	23	74.2	459	2	US-10-280-858A-11	Sequence 11, Appli
436	23	74.2	459	2	US-10-280-858A-13	Sequence 13, Appli
437	23	74.2	459	2	US-10-280-858A-17	Sequence 17, Appli
438	23	74.2	459	2	US-10-280-858A-19	Sequence 19, Appli
439	23	74.2	459	2	US-10-280-858A-21	Sequence 21, Appli
440	23	74.2	459	2	US-10-280-858A-23	Sequence 23, Appli
441	23	74.2	459	2	US-10-280-858A-25	Sequence 25, Appli
442	23	74.2	459	2	US-10-280-858A-27	Sequence 27, Appli
443	23	74.2	459	2	US-10-280-858A-29	Sequence 29, Appli
444	23	74.2	459	2	US-10-280-858A-31	Sequence 31, Appli
445	23	74.2	459	2	US-10-280-858A-33	Sequence 33, Appli
446	23	74.2	459	2	US-10-280-858A-35	Sequence 35, Appli
447	23	74.2	459	2	US-10-280-858A-37	Sequence 37, Appli
448	23	74.2	459	2	US-10-280-858A-39	Sequence 39, Appli
449	23	74.2	459	2	US-10-280-858A-41	Sequence 41, Appli
450	23	74.2	459	2	US-10-280-858A-43	Sequence 43, Appli
451	23	74.2	460	1	US-07-817-920-4	Sequence 4, Appli
452	23	74.2	460	1	US-07-996-772A-9	Sequence 9, Appli
453	23	74.2	460	1	US-08-194-338-13	Sequence 13, Appli
454	23	74.2	460	1	US-08-370-542-4	Sequence 4, Appli
455	23	74.2	460	1	US-08-117-006-4	Sequence 4, Appli
456	23	74.2	460	1	US-08-216-594-4	Sequence 4, Appli
457	23	74.2	460	1	US-08-542-358-4	Sequence 4, Appli
458	23	74.2	460	1	US-09-018-351-4	Sequence 4, Appli
459	23	74.2	460	2	US-09-032-742-4	Sequence 4, Appli
460	23	74.2	460	2	US-09-032-742-20	Sequence 20, Appli
461	23	74.2	460	2	US-09-032-742-23	Sequence 23, Appli
462	23	74.2	460	2	US-09-328-314-18	Sequence 18, Appli
463	23	74.2	460	2	US-09-489-039A-12680	Sequence 12680, A
464	23	74.2	460	5	PCT-US93-00149-4	Sequence 4, Appli

465

23

74.2

461

2

US-09-526-309B-15

Sequence 15, Appli

466

23

74.2

461

2

US-10-280-858A-15

Sequence 15, Appli

467

23

74.2

464

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US-09-902-540-1518

Sequence 1518, A

468

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74.2

475

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US-08-307-444A-1

Sequence 1, Appli

469

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74.2

475

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US-08-307-444A-2

Sequence 2, Appli

470

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74.2

475

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US-08-587-389-1

Sequence 1, Appli

471

23

74.2

475

1

US-08-587-389-2

Sequence 2, Appli

472

23

74.2

476

1

US-08-014-723-1

Sequence 1, Appli

473

23

74.2

476

1

US-08-014-723-2

Sequence 2, Appli

474

23

74.2

476

1

US-08-014-723-18

Sequence 18, Appli

475

23

74.2

476

1

US-08-110-011A-1

Sequence 1, Appli

476

23

74.2

476

1

US-08-110-011A-2

Sequence 2, Appli

477

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74.2

476

1

US-08-110-011A-18

Sequence 18, Appli

478

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74.2

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US-09-252-991A-28020

Sequence 28020, A

479

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74.2

482

2

US-09-252-991A-20129

Sequence 20129, A

480

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74.2

485

2

US-09-949-016-10440

Sequence 10440, A

481

23

74.2

485

2

US-10-094-749-1144

Sequence 1144, Ap

482

23

74.2

488

2

US-09-489-039A-9557

Sequence 9557, Ap

483

23

74.2

492

2

US-09-134-000C-3694

Sequence 3694, Ap

484

23

74.2

494

1

US-08-014-723-14

Sequence 14, Appli

485

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74.2

494

1

US-08-014-723-16

Sequence 16, Appli

486

23

74.2

494

1

US-08-110-011A-14

Sequence 14, Appli

487

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74.2

494

1

US-08-110-011A-16

Sequence 16, Appli

488

23

74.2

497

1

US-08-312-870-3

Sequence 3, Appli

489

23

74.2

497

2

US-09-331-793-4

Sequence 4, Appli

490

23

74.2

498

1

US-08-733-564-2

Sequence 2, Appli

491

23

74.2

503

2

US-09-562-737-66

Sequence 66, Appli

492

23

74.2

508

2

US-09-489-039A-7307

Sequence 7307, Ap

493

23

74.2

516

2

US-09-509-994-1

Sequence 1, Appli

494

23

74.2

516

2

US-09-509-994-2

Sequence 2, Appli

495

23

74.2

536

2

US-09-107-532A-6943

Sequence 6943, Ap

496

23

74.2

536

2

US-09-653-274-10

Sequence 10, Appli

497

23

74.2

541

1

US-10-461-791-19

Sequence 19, Appli

498

23

74.2

546

1

US-08-484-438-6

Sequence 6, Appli

499

23

74.2

542

2

US-09-302-769-14

Sequence 14, Appli

500

23

74.2

542

2

US-09-712-363-180

Sequence 180, Appli

ALIGNMENTS

RESULT 1

US-08-928-862-4

; Sequence 4, Application US/08928862

; Patent No. 6309877

; GENERAL INFORMATION:

; APPLICANT: Chau, Raymond M. W.

; TITLE OF INVENTION: Isolation and Use of Motoneuronotrophic Factors

; FILE REFERENCE: 12592-2

; CURRENT APPLICATION NUMBER: US/08/928, 862

; CURRENT FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 33

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-928-862-4

Query Match

Best Local Similarity 100.0%;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 FSRYAR 6

|||||

Db

17 FSRYAR 22

RESULT 2

US-09-592-018-4

; Sequence 4, Application US/09592018

; Patent No. 6759389

; GENERAL INFORMATION:

APPLICANT: Chau, Raymond M.W.
TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
FILE REFERENCE: 12592-3
CURRENT APPLICATION NUMBER: US/09/592,018
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 33
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-592-018-4

Query Match 100.0%; Score 31; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
17 FSRVAR 22

RESULT 3
US-09-989-481-4
Sequence 4, Application US/09989481
Patent No. 6841531
GENERAL INFORMATION:
APPLICANT: Chau, Raymond M.W.
TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
FILE REFERENCE: 12592-4
CURRENT APPLICATION NUMBER: US/09/989,481
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 09/633,447
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 33
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-989-481-4

Query Match 100.0%; Score 31; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
17 FSRVAR 22

RESULT 4
US-09-198-452A-977
Sequence 977, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 977
LENGTH: 357
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-977

Query Match 100.0%; Score 31; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
135 FSRVAR 140

RESULT 5
US-09-438-185A-906
Sequence 906, Application US/09438185A
Patent No. 682071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 906
LENGTH: 359
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: CPN0904
US-09-438-185A-906

Query Match 100.0%; Score 31; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVAR 6
137 FSRVAR 142

RESULT 6
US-08-914-375C-60
Sequence 60, Application US/08914375C
Patent No. 6377893
GENERAL INFORMATION:
APPLICANT: Steven A. Benner
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESS: Steven A. Benner
STREET: 1501 NW 68th Terrace
CITY: Gainesville
STATE: FL
COUNTRY: United States
ZIP: 32605-4147
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Apple Macintosh

```
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
FILING DATE: 19-AUG-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352 392 7773
TELEFAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: ascb.eco11 6-phospho-strand-glucosidase (E.C. 3.2.1.86
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-08-914-375C-60
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Query Match 100.0%; Score 31; DB 2; Length 466;

Best Local Similarity 100.0%; Pred. No. 82; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 1 FSRVAR 6

Db 154 FSRVAR 159

RESULT 7

US-09-252-991A-23341

Sequence 23341, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23341

LENGTH: 509

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23341

Query Match 100.0%; Score 31; DB 2; Length 509;

Best Local Similarity 100.0%; Pred. No. 90; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 1 FSRVAR 6

Db 270 FSRVAR 275

RESULT 8

US-09-949-016-11070

Sequence 11070, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11070

LENGTH: 188

TYPE: PRT

ORGANISM: Human

US-09-949-016-11070

Query Match 90.3%; Score 28; DB 2; Length 188;

Best Local Similarity 83.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0;

QY 1 FSRVAR 6

Db 83 FSRVAR 88

RESULT 9

US-09-252-991A-18159

Sequence 18159, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18159

LENGTH: 1778

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18159

Query Match 90.3%; Score 28; DB 2; Length 1778;

Best Local Similarity 83.3%; Pred. No. 1.4e+03; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0;

QY 1 FSRVAR 6

Db 1131 FSRVAR 1136

RESULT 10

US-09-252-991A-32051

Sequence 32051, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32051

LENGTH: 198

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32051

Query Match 87.1%; Score 27; DB 2; Length 188;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
Db 94 FSRPAR 99

RESULT 11

US-09-252-991A-19881
; Sequence 19881, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19881
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19881

Query Match 87.1%; Score 27; DB 2; Length 364;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRYAR 6
Db 351 FORYAR 356

RESULT 12
US-09-489-039A-14027
; Sequence 14027, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14027
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14027

Query Match 87.1%; Score 27; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
Db 111 FSRYAQ 116

RESULT 13

US-08-914-375C-61
; Sequence 61, Application US/08914375C
; Patent No. 6377893
; GENERAL INFORMATION:
; APPLICANT: Steven A. Benner
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: 1501 NW 68th Terrace
; CITY: Gainesville
; STATE: FL
; COUNTRY: United States
; ZIP: 32605-4147
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,375C
; FILING DATE: 19-Aug-1997
; CLASSIFICATION: 702/20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352 392 7773
; TELEFAX: 352 331 0462
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; ORIGINAL SOURCE:
; ORGANISM: Etwinia chrysanthemi
; FEATURE:
; OTHER INFORMATION: arbb erwch 6-phospho-strand-glucosidase (E.C. 3.2.1.86
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-08-914-375C-61

Query Match 87.1%; Score 27; DB 2; Length 456;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRYAR 6
Db 150 FERYAR 155

RESULT 14
US-09-198-452A-638
; Sequence 638, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 638
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-638

Query Match 87.1%; Score 27; DB 2; Length 460;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRYAR 6
Db 111 FSRYAQ 116

Db 336 FSRVYR 341

RESULT 15

US-09-489-039A-13505

Sequence 13505, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Bretton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13505

LENGTH: 460

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13505

Query Match 87.1%; Score 27; DB 2; Length 460;

Best Local Similarity 83.3%; Pred. No. 5.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVYR 6

Db 78 FSRVYR 83

RESULT 16

US-09-489-039A-8224

Sequence 8224, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Bretton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8224

LENGTH: 469

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8224

Query Match 87.1%; Score 27; DB 2; Length 469;

Best Local Similarity 83.3%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVYR 6

Db 154 FSRVYR 159

RESULT 17

US-10-026-140-2

Sequence 2, Application US/10026140

Patent No. 7005289

GENERAL INFORMATION:

APPLICANT: Dunn-Coleman, Nigel

APPLICANT: Goedegebuur, Frits

APPLICANT: Ward, Michael

APPLICANT: Yao, Jian

TITLE OF INVENTION: BGL5 Beta-Glucosidase and Nucleic Acids

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: GC697

; CURRENT APPLICATION NUMBER: US/10/026,140

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 484

TYPE: PRT

ORGANISM: Trichoderma reesei

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...((484)

OTHER INFORMATION: Xaa = Any Amino Acid

US-10-026-140-2

Query Match 87.1%; Score 27; DB 3; Length 484;

Best Local Similarity 83.3%; Pred. No. 6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVYR 6

Db 148 FSRVYR 153

RESULT 18

US-09-134-001C-4633

Sequence 4633, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4633

LENGTH: 538

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4633

Query Match 87.1%; Score 27; DB 2; Length 538;

Best Local Similarity 83.3%; Pred. No. 6.7e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVYR 6

Db 77 FSRVYR 82

RESULT 19

US-09-438-185A-599

Sequence 599, Application US/09438185A

Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Stephens, Richard

APPLICANT: Mitchell, Wayne

APPLICANT: Kaiman, Sue

APPLICANT: Davis, Ronald

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US

CURRENT APPLICATION NUMBER: US/09/438,185A

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: US 60/108,279

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: US 60/128,606

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 1074


```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 599
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0597
US-09-438-185A-599

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1 FSRYR 6      |||||
Db      455 FSRYR 460

RESULT 20
US-09-602-787A-548
; Sequence 548, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schüder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US/09-06-23
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
```

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 548
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-548

Query Match      87.1%; Score 27; DB 2; Length 630;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1 FSRYR 6      |||||
Db      105 FSRYR 110

RESULT 21
US-09-949-016-10468
; Sequence 10468, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10468
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10468

Query Match      87.1%; Score 27; DB 2; Length 650;
```

Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FSRVAR 6
Db 283 FSOYAR 288

RESULT 22

US-09-252-991A-29161
; Sequence 29161, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29161
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29161

Query Match 87.1%; Score 27; DB 2; Length 675;
Best Local Similarity 83.3%; Pred. No. 8.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
Db 670 FSRVAR 675

RESULT 23

US-09-543-681A-6306
; Sequence 6306, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6306
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6306

Query Match 83.9%; Score 26; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
Db 46 FSRVAR 51

RESULT 24

US-09-543-681A-6207
; Sequence 6207, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6207
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6207

Query Match 83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
Db 49 FSRVAR 54

RESULT 25

US-08-497-312-20
; Sequence 20, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: Immunoglobulins with reduced immunogenicity of murine
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABAY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 262905
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PMO4UT
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-08-497-312-20

Query Match 83.9%; Score 26; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYA 5
|||
Db 29 FSRYA 33

RESULT 26

US-08-497-312-22
Sequence 22, Application US/08497312

Patent No. 5712120
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Method for obtaining modified immunoglobulins with reduced immunogenicity of murine

TITLE OF INVENTION: antibody variable domains, compositions containing them.

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

STREET: 215 Y 15, ATABEX PLAYA

CITY: HAVANA

STATE:

COUNTRY: CUBA

ZIP: 11600

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/497,312

FILING DATE: 30-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CU 80/94

FILING DATE: 30-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: BOND, LAURENCE B.

REGISTRATION NUMBER: 30,549

REFERENCE/DOCKET NUMBER: 2629US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 801/532-1922

TELEFAX: 801/531-9168

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

US-08-497-312-22

Query Match

Best Local Similarity 83.9%; Score 26; DB 1; Length 119;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYA 5

|||

Db 29 FSRYA 33

RESULT 27

US-08-875-674A-1

Sequence 1, Application US/08875674A

Patent No. 6572857

GENERAL INFORMATION:

APPLICANT: MONTERO CASIMIRO, J. E.

APPLICANT: LOMBARDO VALADARES, J.

APPLICANT: P REZ RODR GUEZ, R.

APPLICANT: SIERRA BL ZQUEZ, P.

APPLICANT: TORO BRAVO, B. R.

TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.

STREET: One Chase Road

CITY: Scarsdale

STATE: New York

COUNTRY: U.S.A.

ZIP: 10583

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).

COMPUTER: Compatible PC IBM (80486, 8 M Ram).

OPERATING SYSTEM: Windows 95.

SOFTWARE: Word Perfect 5.0 for Windows 95.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,674A

FILING DATE: 17-July-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00004

FILING DATE: 18-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: HENRY A. MARZULLO, JR.

REGISTRATION NUMBER: 20,910

REFERENCE/DOCKET NUMBER: P-12

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 723-4300

TELEFAX: (914) 723-4301

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 Amino acid residues.

TYPE: Amino acid.

STRANDEDNESS: Unknown.

TOPOLOGY: Unknown.

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: -N Terminal fragment.

ORIGINAL SOURCE:

ORGANISM: Mice Balb/C

INDIVIDUAL ISOLATE: for t1A

TISSUE TYPE: Murine hybridoma

IMMEDIATE SOURCE:

CLONE: Sub-clone for t1A

FEATURE:

IDENTIFICATION METHOD: Experimental.

OTHER INFORMATION: Sequence corresponding to the variable region

Patent No. 6572857

OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognizing hum.

OTHER INFORMATION: designated as sub-clone for t1A.

US-08-875-674A-1

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 119;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYA 5

|||

Db 29 FSRYA 33

RESULT 28

US-08-875-674A-3

Sequence 3, Application US/08875674A

Patent No. 6572857

GENERAL INFORMATION:

APPLICANT: MONTERO CASIMIRO, J. E.

APPLICANT: LOMBARDO VALADARES, J.

APPLICANT: P REZ RODR GUEZ, R.

APPLICANT: SIERRA BL ZQUEZ, P.

APPLICANT: TORO BRAVO, B. R.

TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.

```

; STREET: One Chase Road
; CITY: Scarsdale
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10583
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
; COMPUTER: Compatible PC IBM (80486, 8 M Ram).
; OPERATING SYSTEM: Windows 95.
; SOFTWARE: Word Perfect 5.0 for Windows 95.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,674A
; FILING DATE: 17-July-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CU96/00004
; FILING DATE: 18-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY A. MARZULLO, JR.
; REGISTRATION NUMBER: 20,910
; REFERENCE/DOCKET NUMBER: P-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 723-4300
; TELEFAX: (914) 723-4301
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 Amino acid residues.
; TYPE: Amino acid.
; STRANDEDNESS: Unknown.
; TOPOLOGY: Unknown.
; MOLECULE TYPE: Protein
; HYPOTHEICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE: -N Terminal fragment.
; ORIGINAL SOURCE:
; TISSUE TYPE: Animal cells.
; CELL LINE: NSO " SP 2/0 " CHO
; IMMEDIATE SOURCE:
; CLONE: Sub-clone for t1A
; FEATURE:
; IDENTIFICATION METHOD: By similarity with known sequence.
; OTHER INFORMATION: Sequence corresponding to the humanized
; Patent No. 6572857
; OTHER INFORMATION: variant of sub-clone for t1A recognizing human CD6, particula
; OTHER INFORMATION: to the variable region of its heavy chain.
; US-08-875-674A-3
;
Query Match      83.9%; Score 26; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FSRVA 5
       |||||
Db      29 FSRVA 33

```

```

RESULT 29
US-10-118-100-51
; Sequence 51, Application US/10118100
; Patent No. 6969250
; GENERAL INFORMATION:
; APPLICANT: Bioinvent International AB
; APPLICANT: Soderlind, Ulf
; APPLICANT: Borreback, Carl
; TITLE OF INVENTION: A Method For In Vitro Molecular
; FILE REFERENCE: Mewburn 341711
; CURRENT APPLICATION NUMBER: US/10/118,100
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/341,711
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: PCT/GB98/00219
; PRIOR FILING DATE: 1998-01-26

```

```

; PRIOR APPLICATION NUMBER: GB9701425.2
; PRIOR FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 51
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: scFv-B11 Antibody Fragment
; US-10-118-100-51

```

```

Query Match      83.9%; Score 26; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FSRVA 5
       |||||
Db      37 FSRVA 41

```

```

RESULT 30
US-09-270-767-44176
; Sequence 44176, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44176
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-44176

```

```

Query Match      83.9%; Score 26; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FSRVA 5
       |||||
Db      96 FSRVA 100

```

```

RESULT 31
US-09-270-767-36842
; Sequence 36842, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36842
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-36842

```

```

Query Match      83.9%; Score 26; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 FSRYA 5
|
|
|
|
Db 55 FSRYA 59

RESULT 32

US-09-270-767-52059
; Sequence 52059, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-034
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 52059
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52059

Query Match 83.9%; Score 26; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FSRYA 5
|
|
|
|
Db 55 FSRYA 59

RESULT 33

US-09-248-528-11
; Sequence 11, Application US/09248528C
; Patent No. 6153415
; GENERAL INFORMATION:
; APPLICANT: Oriel, Patrick J
; APPLICANT: Padmakumar, Rugmini
; APPLICANT: Kim, Sang H
; TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrile
; FILE REFERENCE: MSU 4.1-401
; CURRENT APPLICATION NUMBER: US/09/248,528C
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 60/083,485
; EARLIER FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 229
; TYPE: PRT
; ORGANISM: BR449
US-09-248-528-11

Query Match 83.9%; Score 26; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYA 6
|
|
|
|
Db 161 FPRYAR 166

RESULT 34

US-09-549-108-11
; Sequence 11, Application US/09549108
; Patent No. 6214603
; GENERAL INFORMATION:
; APPLICANT: Oriel, Patrick J

; APPLICANT: Padmakumar, Rugmini
; APPLICANT: Kim, Sang H
; TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrile
; FILE REFERENCE: MSU 4.1-486
; CURRENT APPLICATION NUMBER: US/09/549,108
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/083,485
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 09/248,528
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 229
; TYPE: PRT
; ORGANISM: BR449
US-09-549-108-11

Query Match 83.9%; Score 26; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYA 6
|
|
|
|
Db 161 FPRYAR 166

RESULT 35

US-09-549-111-11
; Sequence 11, Application US/09549111
; Patent No. 6228633
; GENERAL INFORMATION:
; APPLICANT: Oriel, Patrick J
; APPLICANT: Padmakumar, Rugmini
; APPLICANT: Kim, Sang H
; TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrile
; FILE REFERENCE: MSU 4.1-489
; CURRENT APPLICATION NUMBER: US/09/549,111
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/083,485
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 09/248,528
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 229
; TYPE: PRT
; ORGANISM: BR449
US-09-549-111-11

Query Match 83.9%; Score 26; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYA 6
|
|
|
|
Db 161 FPRYAR 166

RESULT 36

US-09-549-106-11
; Sequence 11, Application US/09549106
; Patent No. 6242242
; GENERAL INFORMATION:
; APPLICANT: Oriel, Patrick J
; APPLICANT: Padmakumar, Rugmini
; APPLICANT: Kim, Sang H
; TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrile
; FILE REFERENCE: MSU 4.1-487

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; CURRENT APPLICATION NUMBER: US/09/549,106
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/083,485
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 09/248,528
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 229
; TYPE: PRT
; ORGANISM: BR449
US-09-549-106-11

Query Match      83.9%; Score 26; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      161 FPRVAR 166

RESULT 37
US-09-550-394-11
; Sequence 11, Application US/09550394
; Patent No. 6287828
; GENERAL INFORMATION:
; APPLICANT: Oriol, Patrick J
; APPLICANT: Padmakumar, Ruggini
; APPLICANT: Kim, Sang H
; TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrite
; TITLE OF INVENTION: Hydrazide from a Thermophilic Bacillus
; FILE REFERENCE: MSU 4.1-488
; CURRENT APPLICATION NUMBER: US/09/550,394
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/083,485
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 09/248,528
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 229
; TYPE: PRT
; ORGANISM: BR449
US-09-550-394-11

Query Match      83.9%; Score 26; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      161 FPRVAR 166

RESULT 38
US-09-489-039A-12718
; Sequence 12718, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12718
; LENGTH: 233
```

```
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12718

Query Match      83.9%; Score 26; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRYA 5
        |||||
Db      138 FSRYA 142

RESULT 39
US-09-949-016-6472
; Sequence 6472, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6472
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6472

Query Match      83.9%; Score 26; DB 2; Length 252;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      240 FSRVAR 245

RESULT 40
US-09-949-016-9375
; Sequence 9375, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9375
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9375

Query Match      83.9%; Score 26; DB 2; Length 253;
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Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 241 FSRYAR 246

RESULT 41

US-09-198-452A-266
; Sequence 266, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 266
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-266

Query Match 83.9%; Score 26; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYA 5
Db 150 FSRYA 154

RESULT 42

US-09-438-185A-256
; Sequence 256, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 256
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPH0254
US-09-438-185A-256

Query Match 83.9%; Score 26; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYA 5
Db 150 FSRYA 154

RESULT 43
US-09-252-991A-25159
; Sequence 25159, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25159
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25159

Query Match 83.9%; Score 26; DB 2; Length 276;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 71 FSRYAR 76

RESULT 44

US-09-252-991A-20485
; Sequence 20485, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20485
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20485

Query Match 83.9%; Score 26; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
Db 64 FSRYAR 69

RESULT 45

US-08-944-483-66
; Sequence 66, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.
APPLICANT: STROPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-66

Query Match 83.9%; Score 26; DB 2; Length 299;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 102 FSRYIR 107

RESULT 46
US-09-248-796A-14594
Sequence 14594, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14594
LENGTH: 308
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-14594

Query Match 83.9%; Score 26; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYA 5
Db 190 FSRYA 194

RESULT 47
US-09-386-642-12
Sequence 12, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 319
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
US-09-386-642-12

Query Match 83.9%; Score 26; DB 2; Length 319;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 144 FSRYIR 149

RESULT 48
US-09-489-039A-14005
Sequence 14005, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14005
LENGTH: 327
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14005

Query Match 83.9%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRYAR 6
Db 251 WSRYAR 256

RESULT 49
US-09-386-642-11
Sequence 11, Application US/09386642


```
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11
```

```
Query Match      83.9%; Score 26; DB 2; Length 328;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 FSRYAR 6
        |||||
Db      153 FSRYLR 158
```

```
RESULT 50
US-09-438-185A-960
; Sequence 960, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 960
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0958
US-09-438-185A-960
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Query Match      83.9%; Score 26; DB 2; Length 337;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 FSRYAR 6
        |||||
Db      9 FSRYLR 14
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Search completed: August 29, 2006, 06:17:52
Job time : 14.3366 secs
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102	27	87.1	412	5	US-10-732-923-22297	Sequence 22297, A	175	27	87.1	837	4	US-10-437-963-132655	Sequence 132655
103	27	87.1	414	5	US-10-511-698-37	Sequence 37, App1	176	27	87.1	1027	4	US-10-437-963-137165	Sequence 137165
104	27	87.1	420	4	US-10-425-115-365824	Sequence 365824, A	177	26	83.9	10	4	US-10-031-8744-98	Sequence 98, App1
105	27	87.1	425	5	US-10-732-923-22291	Sequence 22291, A	178	26	83.9	10	4	US-10-031-8744-101	Sequence 101, App1
106	27	87.1	428	5	US-10-511-698-38	Sequence 38, App1	179	26	83.9	39	4	US-10-424-599-153126	Sequence 153126
107	27	87.1	445	4	US-10-097-111-289	Sequence 289, App	180	26	83.9	42	4	US-10-425-115-359594	Sequence 359594
108	27	87.1	453	4	US-10-369-493-14065	Sequence 14065, A	181	26	83.9	49	5	US-10-467-657-2278	Sequence 2278, Ap
109	27	87.1	456	4	US-10-282-122A-74836	Sequence 74836, A	182	26	83.9	50	4	US-10-424-599-263997	Sequence 263997, A
110	27	87.1	456	4	US-10-282-122A-75400	Sequence 75400, A	183	26	83.9	50	4	US-10-428-275-86	Sequence 86, App1
111	27	87.1	456	6	US-11-087-099-5433	Sequence 5433, Ap	184	26	83.9	66	4	US-10-424-599-184533	Sequence 184533
112	27	87.1	456	6	US-11-087-099-6176	Sequence 6176, Ap	185	26	83.9	66	4	US-10-425-115-209804	Sequence 209804
113	27	87.1	456	6	US-11-188-298-16004	Sequence 16004, A	186	26	83.9	72	4	US-10-424-599-265076	Sequence 265076
114	27	87.1	457	4	US-10-369-493-729	Sequence 729, App	187	26	83.9	82	4	US-10-424-599-274595	Sequence 274595
115	27	87.1	457	4	US-10-282-122A-43084	Sequence 43084, A	188	26	83.9	89	4	US-10-767-701-52537	Sequence 52537, A
116	27	87.1	457	4	US-10-282-122A-60097	Sequence 60097, A	189	26	83.9	104	3	US-09-764-848-28	Sequence 28, App1
117	27	87.1	457	6	US-11-087-099-2494	Sequence 2494, Ap	190	26	83.9	104	3	US-09-764-875-1132	Sequence 1132, Ap
118	27	87.1	457	6	US-11-087-099-3478	Sequence 3478, Ap	191	26	83.9	104	4	US-10-116-016-28	Sequence 28, App1
119	27	87.1	457	6	US-11-188-298-2380	Sequence 2380, Ap	192	26	83.9	104	4	US-10-222-020-28	Sequence 28, App1
120	27	87.1	457	6	US-11-188-298-3280	Sequence 3280, Ap	193	26	83.9	108	4	US-10-424-599-173271	Sequence 173271
121	27	87.1	458	6	US-11-087-099-9639	Sequence 9639, Ap	194	26	83.9	108	6	US-11-087-099-4881	Sequence 4881, A
122	27	87.1	458	6	US-11-087-099-11216	Sequence 11216, A	195	26	83.9	109	6	US-11-096-568A-13389	Sequence 13389, A
123	27	87.1	458	6	US-11-188-298-8947	Sequence 8947, Ap	196	26	83.9	113	4	US-10-437-963-128432	Sequence 128432
124	27	87.1	458	6	US-11-188-298-10343	Sequence 10343, A	197	26	83.9	119	6	US-11-049-536-370	Sequence 370, App
125	27	87.1	460	4	US-10-289-762-638	Sequence 762, App	198	26	83.9	119	6	US-11-199-739-370	Sequence 370, App
126	27	87.1	463	3	US-09-815-242-13918	Sequence 13918, A	199	26	83.9	120	6	US-11-049-536-518	Sequence 518, App
127	27	87.1	463	4	US-10-369-493-314	Sequence 314, App	200	26	83.9	120	6	US-11-199-739-518	Sequence 518, App
128	27	87.1	463	4	US-10-282-122A-78313	Sequence 78313, A	201	26	83.9	121	4	US-10-415-478A-64	Sequence 64, App1
129	27	87.1	463	6	US-11-087-099-7201	Sequence 7201, Ap	202	26	83.9	121	5	US-10-472-928-094	Sequence 2094, Ap
130	27	87.1	463	6	US-11-087-099-11335	Sequence 11335, A	203	26	83.9	125	3	US-09-828-708-14	Sequence 14, App1
131	27	87.1	463	6	US-11-188-298-6612	Sequence 6612, Ap	204	26	83.9	125	4	US-10-425-115-283844	Sequence 283844
132	27	87.1	463	6	US-11-188-298-21475	Sequence 21475, A	205	26	83.9	125	5	US-10-630-009-14	Sequence 14, App1
133	27	87.1	472	6	US-11-087-099-13391	Sequence 12391, A	206	26	83.9	127	4	US-10-714-353-6	Sequence 6, App1
134	27	87.1	472	6	US-11-188-298-11371	Sequence 11371, A	207	26	83.9	128	4	US-10-424-599-155954	Sequence 155954
135	27	87.1	478	4	US-10-369-493-16830	Sequence 16830, A	208	26	83.9	130	4	US-10-118-100-51	Sequence 51, App1
136	27	87.1	478	6	US-11-188-298-18308	Sequence 18308, A	209	26	83.9	130	6	US-11-109-264-51	Sequence 51, App1
137	27	87.1	483	4	US-10-369-493-14243	Sequence 14243, A	210	26	83.9	132	4	US-10-767-701-43324	Sequence 43324, A
138	27	87.1	484	6	US-10-026-140-2	Sequence 2, App1	211	26	83.9	135	4	US-10-425-115-10189	Sequence 210389
139	27	87.1	484	6	US-11-147-725-2	Sequence 2, App1	212	26	83.9	137	4	US-10-425-115-335852	Sequence 335852
140	27	87.1	485	6	US-11-087-099-9429	Sequence 9429, Ap	213	26	83.9	137	4	US-10-006-773-4	Sequence 4, App1
141	27	87.1	485	6	US-11-188-298-19761	Sequence 19761, A	214	26	83.9	140	4	US-10-467-657-4246	Sequence 4246, Ap
142	27	87.1	488	3	US-09-981-900B-7	Sequence 7, App1	215	26	83.9	145	5	US-10-425-115-22327	Sequence 22327, A
143	27	87.1	491	4	US-10-282-122A-69578	Sequence 69578, A	216	26	83.9	151	4	US-10-106-698-6779	Sequence 6779, Ap
144	27	87.1	502	4	US-10-156-761-11329	Sequence 11329, A	217	26	83.9	169	4	US-10-369-493-2230	Sequence 2230, Ap
145	27	87.1	505	4	US-10-369-493-14505	Sequence 14505, A	218	26	83.9	174	4	US-10-369-493-2230	Sequence 2230, Ap
146	27	87.1	505	4	US-10-369-493-14906	Sequence 14906, A	219	26	83.9	185	4	US-10-425-115-113775	Sequence 311725
147	27	87.1	538	4	US-10-724-972A-4824	Sequence 4824, Ap	220	26	83.9	189	5	US-10-467-657-4524	Sequence 4524, Ap
148	27	87.1	541	4	US-10-424-599-171116	Sequence 171116, A	221	26	83.9	198	5	US-10-450-753-32783	Sequence 32783, A
149	27	87.1	545	4	US-10-425-114-45091	Sequence 45091, A	222	26	83.9	211	4	US-10-424-599-240815	Sequence 240815
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151	27	87.1	579	4	US-10-359-289-2	Sequence 2, App1	224	26	83.9	219	6	US-11-096-568A-16580	Sequence 16580, A
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154	27	87.1	592	5	US-10-732-923-22125	Sequence 22125, A	227	26	83.9	231	3	US-09-898-837A-43	Sequence 43, App1
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156	27	87.1	607	4	US-10-369-493-12204	Sequence 12204, A	229	26	83.9	234	3	US-09-898-837A-48	Sequence 48, App1
157	27	87.1	608	4	US-10-369-493-12230	Sequence 12230, A	230	26	83.9	241	4	US-10-156-761-214640	Sequence 14640, A
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159	27	87.1	630	3	US-09-738-625-6059	Sequence 6059, Ap	232	26	83.9	247	3	US-09-880-748-878	Sequence 878, App
160	27	87.1	630	4	US-10-627-476-548	Sequence 548, App	233	26	83.9	247	3	US-09-880-748-1090	Sequence 1090, Ap
161	27	87.1	635	5	US-10-494-672-298	Sequence 298, App	234	26	83.9	247	3	US-09-880-748-1099	Sequence 1099, Ap
162	27	87.1	647	5	US-10-732-923-22114	Sequence 22114, A	235	26	83.9	247	4	US-09-880-748-1328	Sequence 1328, Ap
163	27	87.1	648	5	US-10-732-923-22116	Sequence 22116, A	236	26	83.9	247	4	US-10-293-418-878	Sequence 878, App
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165	27	87.1	650	4	US-10-408-713-10	Sequence 10, App1	238	26	83.9	247	4	US-10-229-418-1328	Sequence 1099, Ap
166	27	87.1	650	5	US-10-732-923-22282	Sequence 22282, A	239	26	83.9	247	4	US-10-229-418-1328	Sequence 1328, Ap
167	27	87.1	650	5	US-10-732-923-22283	Sequence 22283, A	240	26	83.9	247	6	US-11-054-515-878	Sequence 878, App
168	27	87.1	650	5	US-10-732-923-22284	Sequence 22284, A	241	26	83.9	247	6	US-11-054-515-1090	Sequence 1090, Ap
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170	27	87.1	650	5	US-10-732-923-22294	Sequence 22294, A	243	26	83.9	247	6	US-11-054-515-1328	Sequence 1328, Ap
171	27	87.1	650	5	US-10-756-149-4983	Sequence 4983, Ap	244	26	83.9	247	6	US-11-266-444-878	Sequence 878, App
172	27	87.1	650	5	US-10-511-698-36	Sequence 36, App1	245	26	83.9	247	6	US-11-266-444-1090	Sequence 1090, Ap
173	27	87.1	672	4	US-10-346-863-10	Sequence 10, App1	246	26	83.9	247	6	US-11-266-444-1099	Sequence 1099, Ap

247	26	83.9	247	6	US-11-266-444-1328	Sequence 1328, Ap	320	26	83.9	343	5	US-10-784-004-661	Sequence 661, App
248	26	83.9	249	3	US-09-815-242-10880	Sequence 10880, A	321	26	83.9	343	5	US-10-784-004-663	Sequence 663, App
249	26	83.9	250	3	US-11-087-099-1459	Sequence 1459, Ap	322	26	83.9	343	5	US-10-784-004-1060	Sequence 1060, Ap
250	26	83.9	251	3	US-09-925-301-1050	Sequence 1050, Ap	323	26	83.9	343	6	US-11-017-119-2	Sequence 2, Appl1
251	26	83.9	251	4	US-10-767-701-45303	Sequence 45303, A	324	26	83.9	343	6	US-11-050-926-262	Sequence 262, App
252	26	83.9	252	4	US-10-087-192-1242	Sequence 1242, Ap	325	26	83.9	343	6	US-11-080-591-86	Sequence 86, Appl1
253	26	83.9	253	3	US-09-880-748-1199	Sequence 1199, Ap	326	26	83.9	343	6	US-11-019-711-130	Sequence 130, App
254	26	83.9	254	4	US-10-293-418-1199	Sequence 1199, Ap	327	26	83.9	348	5	US-10-470-0488-72	Sequence 72, Appl1
255	26	83.9	255	6	US-11-054-515-1199	Sequence 1199, Ap	328	26	83.9	349	5	US-10-739-930-9327	Sequence 9327, Ap
256	26	83.9	256	6	US-11-266-444-1199	Sequence 1199, Ap	329	26	83.9	350	4	US-10-424-599-188274	Sequence 182374, A
257	26	83.9	257	3	US-09-880-748-1012	Sequence 1012, Ap	330	26	83.9	356	4	US-10-369-493-3321	Sequence 3321, A
258	26	83.9	258	4	US-10-293-418-1012	Sequence 1012, Ap	331	26	83.9	355	3	US-09-995-493-22	Sequence 22, Appl1
259	26	83.9	259	6	US-11-054-515-1012	Sequence 1012, Ap	332	26	83.9	377	6	US-11-096-568A-16578	Sequence 16578, A
260	26	83.9	260	6	US-11-266-444-1012	Sequence 1012, Ap	333	26	83.9	386	4	US-10-042-865-32	Sequence 32, Appl1
261	26	83.9	261	4	US-10-289-762-266	Sequence 266, App	334	26	83.9	393	5	US-10-821-234-1043	Sequence 1043, Ap
262	26	83.9	262	4	US-10-479-670-192	Sequence 192, App	335	26	83.9	395	4	US-10-437-963-15167	Sequence 15167, A
263	26	83.9	263	4	US-10-425-115-282322	Sequence 282322, A	336	26	83.9	407	5	US-10-732-923-17540	Sequence 17540, A
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266	26	83.9	266	4	US-10-425-115-210385	Sequence 210385, A	339	26	83.9	435	4	US-10-074-566-18	Sequence 18, Appl1
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268	26	83.9	268	6	US-11-087-099-2401	Sequence 2401, Ap	341	26	83.9	448	4	US-10-282-122A-72853	Sequence 72853, A
269	26	83.9	269	6	US-11-087-099-4667	Sequence 4667, Ap	342	26	83.9	450	4	US-10-369-493-19569	Sequence 19569, A
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271	26	83.9	271	6	US-11-087-099-5782	Sequence 5782, Ap	344	26	83.9	451	4	US-10-428-275-100	Sequence 100, Appl1
272	26	83.9	272	6	US-11-087-099-7730	Sequence 7730, Ap	345	26	83.9	451	4	US-10-428-275-102	Sequence 102, App
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285	26	83.9	285	6	US-11-096-568A-23462	Sequence 23462, Ap	358	26	83.9	509	5	US-10-470-0488-672	Sequence 67, Appl1
286	26	83.9	286	6	US-10-774-355A-1505	Sequence 1505, Ap	359	26	83.9	520	4	US-10-128-714-8505	Sequence 3505, Ap
287	26	83.9	287	6	US-10-168-663-15	Sequence 15, Appl1	360	26	83.9	528	4	US-10-128-714-8505	Sequence 8505, Ap
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291	26	83.9	291	5	US-10-015-989A-11	Sequence 11, Appl1	364	26	83.9	547	4	US-10-377-072-2	Sequence 2, Appl1
292	26	83.9	292	3	US-09-764-875-844	Sequence 844, App	365	26	83.9	549	5	US-10-462-706-1-197	Sequence 17, App
293	26	83.9	293	3	US-09-833-245-191	Sequence 191, App	366	26	83.9	557	5	US-10-369-493-3398	Sequence 3398, Ap
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295	26	83.9	295	6	US-11-264-096-191	Sequence 191, App	368	26	83.9	571	3	US-09-833-245-1090	Sequence 1090, Ap
296	26	83.9	296	4	US-10-109-616-2	Sequence 2, Appl1	369	26	83.9	571	3	US-10-036-342-23	Sequence 23, Appl1
297	26	83.9	297	4	US-10-042-865-153	Sequence 153, App	370	26	83.9	571	4	US-10-036-342-23	Sequence 23, Appl1
298	26	83.9	298	4	US-10-724-972A-5121	Sequence 5121, Ap	371	26	83.9	571	4	US-10-028-072-542	Sequence 542, App
299	26	83.9	299	4	US-10-051-874-86	Sequence 86, Appl1	372	26	83.9	571	4	US-10-035-855-23	Sequence 23, Appl1
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302	26	83.9	302	4	US-10-042-865-152	Sequence 152, App	375	26	83.9	571	4	US-10-121-049-542	Sequence 542, App
303	26	83.9	303	4	US-10-042-865-154	Sequence 154, App	376	26	83.9	571	4	US-10-123-904-542	Sequence 542, App
304	26	83.9	304	4	US-10-425-114-36811	Sequence 36811, A	377	26	83.9	571	4	US-10-140-470-542	Sequence 542, App
305	26	83.9	305	4	US-10-037-417-133	Sequence 133, App	378	26	83.9	571	4	US-10-175-746-542	Sequence 542, App
306	26	83.9	306	4	US-10-037-417-134	Sequence 134, App	379	26	83.9	571	4	US-10-176-921-542	Sequence 542, App
307	26	83.9	307	5	US-10-784-004-341	Sequence 341, App	380	26	83.9	571	4	US-10-16-921-542	Sequence 542, App
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313	26	83.9	313	4	US-10-176-847-86	Sequence 86, Appl1	386	26	83.9	571	4	US-10-143-131-542	Sequence 542, App
314	26	83.9	314	4	US-10-097-340-362	Sequence 362, App	387	26	83.9	571	4	US-10-143-131-542	Sequence 542, App
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319	26	83.9	319	4	US-10-712-124-8	Sequence 8, Appl1	392	26	83.9	571	4	US-10-218-631-210	Sequence 210, App

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199	26	83.9	571	US-10-141-755-542	Sequence 542, App	472	26	83.9	571	4	US-10-128-690A-542	Sequence 542, App							
400	26	83.9	571	US-10-143-032-542	Sequence 542, App	473	26	83.9	571	4	US-10-128-691A-542	Sequence 542, App							
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403	26	83.9	571	US-10-123-236-542	Sequence 542, App	476	26	83.9	571	4	US-10-131-836A-542	Sequence 542, App							
404	26	83.9	571	US-10-123-261-542	Sequence 542, App	477	26	83.9	571	4	US-10-146-729-542	Sequence 542, App							
405	26	83.9	571	US-10-140-921-542	Sequence 542, App	478	26	83.9	571	4	US-10-146-791-542	Sequence 542, App							
406	26	83.9	571	US-10-140-928-542	Sequence 542, App	479	26	83.9	571	4	US-10-147-484-542	Sequence 542, App							
407	26	83.9	571	US-10-216-159A-210	Sequence 210, App	480	26	83.9	571	4	US-10-147-508-542	Sequence 542, App							
408	26	83.9	571	US-10-121-045-542	Sequence 542, App	481	26	83.9	571	4	US-10-147-512-542	Sequence 542, App							
409	26	83.9	571	US-10-123-292-542	Sequence 542, App	482	26	83.9	571	4	US-10-175-735-542	Sequence 542, App							
410	26	83.9	571	US-10-123-903-542	Sequence 542, App	483	26	83.9	571	4	US-10-121-040-542	Sequence 542, App							
411	26	83.9	571	US-10-124-819-542	Sequence 542, App	484	26	83.9	571	4	US-10-121-056-542	Sequence 542, App							
412	26	83.9	571	US-10-124-822-542	Sequence 542, App	485	26	83.9	571	4	US-10-121-061-542	Sequence 542, App							
413	26	83.9	571	US-10-140-925-542	Sequence 542, App	486	26	83.9	571	4	US-10-123-235-542	Sequence 542, App							
414	26	83.9	571	US-10-160-498-542	Sequence 542, App	487	26	83.9	571	4	US-10-124-818-542	Sequence 542, App							
415	26	83.9	571	US-10-218-849-210	Sequence 210, App	488	26	83.9	571	4	US-10-137-868-542	Sequence 542, App							
416	26	83.9	571	US-10-227-873-210	Sequence 210, App	489	26	83.9	571	4	US-10-147-692-542	Sequence 542, App							
417	26	83.9	571	US-10-227-883-210	Sequence 210, App	490	26	83.9	571	4	US-10-158-782-542	Sequence 542, App							
418	26	83.9	571	US-10-124-824-542	Sequence 542, App	491	26	83.9	571	4	US-10-133-905-542	Sequence 542, App							
419	26	83.9	571	US-10-127-825A-542	Sequence 542, App	492	26	83.9	571	4	US-10-123-907-542	Sequence 542, App							
420	26	83.9	571	US-10-127-829A-542	Sequence 542, App	493	26	83.9	571	4	US-10-124-815-542	Sequence 542, App							
421	26	83.9	571	US-10-127-835A-542	Sequence 542, App	494	26	83.9	571	4	US-10-125-921A-542	Sequence 542, App							
422	26	83.9	571	US-10-127-839A-542	Sequence 542, App	495	26	83.9	571	4	US-10-125-928A-542	Sequence 542, App							
423	26	83.9	571	US-10-127-901A-542	Sequence 542, App	496	26	83.9	571	4	US-10-127-821A-542	Sequence 542, App							
424	26	83.9	571	US-10-128-693A-542	Sequence 542, App	497	26	83.9	571	4	US-10-127-822A-542	Sequence 542, App							
425	26	83.9	571	US-10-131-813A-542	Sequence 542, App	498	26	83.9	571	4	US-10-127-824A-542	Sequence 542, App							
426	26	83.9	571	US-10-131-818A-542	Sequence 542, App	499	26	83.9	571	4	US-10-127-826A-542	Sequence 542, App							
427	26	83.9	571	US-10-131-823A-542	Sequence 542, App	500	26	83.9	571	4	US-10-127-827A-542	Sequence 542, App							
428	26	83.9	571	US-10-131-824A-542	Sequence 542, App	ALIGNMENTS													
429	26	83.9	571	US-10-131-830A-542	Sequence 542, App														
430	26	83.9	571	US-10-131-837A-542	Sequence 542, App														
431	26	83.9	571	US-10-131-872A-542	Sequence 542, App														
432	26	83.9	571	US-10-147-500-542	Sequence 542, App														
433	26	83.9	571	US-10-147-502-542	Sequence 542, App														
434	26	83.9	571	US-10-147-515-542	Sequence 542, App														
435	26	83.9	571	US-10-147-517-542	Sequence 542, App														
436	26	83.9	571	US-10-147-526-542	Sequence 542, App														
437	26	83.9	571	US-10-147-527-542	Sequence 542, App														
438	26	83.9	571	US-10-121-041-542	Sequence 542, App	RESULT 1													
439	26	83.9	571	US-10-121-043-542	Sequence 542, App														
440	26	83.9	571	US-10-121-047-542	Sequence 542, App														
441	26	83.9	571	US-10-123-215-542	Sequence 542, App														
442	26	83.9	571	US-10-123-902-542	Sequence 542, App														
443	26	83.9	571	US-10-123-908-542	Sequence 542, App														
444	26	83.9	571	US-10-123-909-542	Sequence 542, App														
445	26	83.9	571	US-10-123-910-542	Sequence 542, App														
446	26	83.9	571	US-10-124-813-542	Sequence 542, App														
447	26	83.9	571	US-10-124-817-542	Sequence 542, App														
448	26	83.9	571	US-10-125-922-542	Sequence 542, App	US-10-541-343-2													
449	26	83.9	571	US-10-125-924-542	Sequence 542, App														
450	26	83.9	571	US-10-140-860-542	Sequence 542, App														
451	26	83.9	571	US-10-143-417-542	Sequence 542, App														
452	26	83.9	571	US-10-147-519-542	Sequence 542, App														
453	26	83.9	571	US-10-157-782-542	Sequence 542, App														
454	26	83.9	571	US-10-152-395-542	Sequence 542, App														
455	26	83.9	571	US-10-219-076-210	Sequence 210, App														
456	26	83.9	571	US-10-230-434-210	Sequence 210, App														
457	26	83.9	571	US-10-125-926A-542	Sequence 542, App														
458	26	83.9	571	US-10-125-930A-542	Sequence 542, App	US-10-541-343-2													
459	26	83.9	571	US-10-127-831A-542	Sequence 542, App														
460	26	83.9	571	US-10-127-837A-542	Sequence 542, App														
461	26	83.9	571	US-10-127-838B-542	Sequence 542, App														
462	26	83.9	571	US-10-127-842A-542	Sequence 542, App														
463	26	83.9	571	US-10-127-843A-542	Sequence 542, App														
464	26	83.9	571	US-10-127-845A-542	Sequence 542, App														
465	26	83.9	571	US-10-127-846A-542	Sequence 542, App														
Query Match 100.0%; Score 31; DB 5; Length 6;																			
Best Local Similarity 100.0%; Pred. No. 1.9e+06; Indels 0; Gaps 0;																			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																			
1 FSRAR 6																			
1 FSRAR 6																			
Db																			

RESULT 2
US-10-541-343-4
; Sequence 4, Application US/10541343
; Publication No. US20060052299A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond Ming Wah
; APPLICANT: Ko, Pui-Yuk Dorothy
; TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
; FILE REFERENCE: 2001-103US
; CURRENT APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: PCT/US2004/001468
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,722
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-541-343-4

Query Match 100.0%; Score 31; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|||
Db 5 FSRYAR 10

RESULT 3
US-10-541-343-5
; Sequence 5, Application US/10541343
; Publication No. US20060052299A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond Ming Wah
; APPLICANT: Ko, Pui-Yuk Dorothy
; TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
; FILE REFERENCE: 2001-103US
; CURRENT APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: PCT/US2004/001468
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,722
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-541-343-5

Query Match 100.0%; Score 31; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|||
Db 1 FSRYAR 6

RESULT 4
US-10-541-343-6
; Sequence 6, Application US/10541343
; Publication No. US20060052299A1

; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond Ming Wah
; APPLICANT: Ko, Pui-Yuk Dorothy
; TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
; FILE REFERENCE: 2001-103US
; CURRENT APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: PCT/US2004/001468
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,722
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-541-343-6

Query Match 100.0%; Score 31; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|||
Db 7 FSRYAR 12

RESULT 5
US-10-541-343-7
; Sequence 7, Application US/10541343
; Publication No. US20060052299A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond Ming Wah
; APPLICANT: Ko, Pui-Yuk Dorothy
; TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
; FILE REFERENCE: 2001-103US
; CURRENT APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: PCT/US2004/001468
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,722
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-541-343-7

Query Match 100.0%; Score 31; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYAR 6
|||
Db 5 FSRYAR 10

RESULT 6
US-09-989-481-4
; Sequence 4, Application US/09989481
; Publication No. US20020096831A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-4
; CURRENT APPLICATION NUMBER: US/09/989,481

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/ CURRENT FILING DATE: 2001-11-20
/ PRIOR APPLICATION NUMBER: US 09/633,447
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 08/9928862
/ PRIOR FILING DATE: 1997-09-12
/ PRIOR APPLICATION NUMBER: US 08/751225
/ PRIOR FILING DATE: 1996-11-15
/ PRIOR APPLICATION NUMBER: US 60/026792
/ PRIOR FILING DATE: 1996-09-27
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-989-481-4

Query Match          100.0%; Score 31; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRVAR 6
        |||||
Db      17 FSRVAR 22

RESULT 7
US-10-858-545-4
/ Sequence 4, Application US/10858545
/ Publication No. US20040224894A1
/ GENERAL INFORMATION:
/ APPLICANT: Chau, Raymond M.W.
/ TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
/ FILE REFERENCE: 12592-3
/ CURRENT APPLICATION NUMBER: US/10/858,545
/ CURRENT FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US/09/592,018
/ PRIOR FILING DATE: 2000-06-12
/ PRIOR APPLICATION NUMBER: US 08/9928862
/ PRIOR FILING DATE: 1997-09-12
/ PRIOR APPLICATION NUMBER: US 08/751225
/ PRIOR FILING DATE: 1996-11-15
/ PRIOR APPLICATION NUMBER: US 60/026792
/ PRIOR FILING DATE: 1996-09-27
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-858-545-4

Query Match          100.0%; Score 31; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRVAR 6
        |||||
Db      17 FSRVAR 22

RESULT 8
US-10-858-286-4
/ Sequence 4, Application US/10858286
/ Publication No. US20040242486A1
/ GENERAL INFORMATION:
/ APPLICANT: Chau, Raymond M.W.
/ TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
/ FILE REFERENCE: 12592-3
/ CURRENT APPLICATION NUMBER: US/10/858,286
/ CURRENT FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US/09/592,018
/ PRIOR FILING DATE: 2000-06-12
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/ PRIOR APPLICATION NUMBER: US 08/9928862
/ PRIOR FILING DATE: 1997-09-12
/ PRIOR APPLICATION NUMBER: US 08/751225
/ PRIOR FILING DATE: 1996-11-15
/ PRIOR APPLICATION NUMBER: US 60/026792
/ PRIOR FILING DATE: 1996-09-27
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-858-286-4

Query Match          100.0%; Score 31; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRVAR 6
        |||||
Db      17 FSRVAR 22

RESULT 9
US-10-858-543-4
/ Sequence 4, Application US/10858543
/ Publication No. US2004026691A1
/ GENERAL INFORMATION:
/ APPLICANT: Chau, Raymond M.W.
/ TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
/ FILE REFERENCE: 12592-3
/ CURRENT APPLICATION NUMBER: US/10/858,543
/ CURRENT FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US/09/592,018
/ PRIOR FILING DATE: 2000-06-12
/ PRIOR APPLICATION NUMBER: US 08/9928862
/ PRIOR FILING DATE: 1997-09-12
/ PRIOR APPLICATION NUMBER: US 08/751225
/ PRIOR FILING DATE: 1996-11-15
/ PRIOR APPLICATION NUMBER: US 60/026792
/ PRIOR FILING DATE: 1996-09-27
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-858-543-4

Query Match          100.0%; Score 31; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRVAR 6
        |||||
Db      17 FSRVAR 22

RESULT 10
US-10-858-144-4
/ Sequence 4, Application US/10858144
/ Publication No. US2006002565A1
/ GENERAL INFORMATION:
/ APPLICANT: Chau, Raymond M.W.
/ TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
/ FILE REFERENCE: 12592-3
/ CURRENT APPLICATION NUMBER: US/10/858,144
/ CURRENT FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US/09/592,018
/ PRIOR FILING DATE: 2000-06-12
/ PRIOR APPLICATION NUMBER: US 08/9928862
/ PRIOR FILING DATE: 1997-09-12
/ PRIOR APPLICATION NUMBER: US 08/751225
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PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 33
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-858-144-4

Query Match 100.0%; Score 31; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 17 FSRVAR 22

RESULT 11
US-10-541-343-1
Sequence 1, Application US/10541343
Publication No. US20060052299A1
GENERAL INFORMATION:
APPLICANT: Chau, Raymond Ming Mah
TITLE OF INVENTION: NMTF Peptides and Compositions and Methods of Use
FILE REFERENCE: 2001-103US
CURRENT APPLICATION NUMBER: US/10/541,343
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 33
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-541-343-1

Query Match 100.0%; Score 31; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 17 FSRVAR 22

RESULT 12
US-11-188-298-11746
Sequence 11746, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USFS FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 11746
LENGTH: 125
TYPE: PRT
ORGANISM: Desulfotobacterium hafniense
US-11-188-298-11746

Query Match 100.0%; Score 31; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 76 FSRVAR 81

RESULT 13
US-10-312-273-107
Sequence 107, Application US/10312273
Publication No. US20040005667A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
FILE REFERENCE: P025035WO
CURRENT APPLICATION NUMBER: US/10/312,273
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 0016363.4
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 0017047.2
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 0017983.8
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 0019368.0
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 0020440.4
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 0022583.9
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 0027549.5
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 0031706.5
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 664
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 107
LENGTH: 357
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-10-312-273-107

Query Match 100.0%; Score 31; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 135 FSRVAR 140

RESULT 14
US-10-289-762-977
Sequence 977, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Grifflais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 977
LENGTH: 357
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-10-289-762-977

Query Match 100.0%; Score 31; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FSRVAR 6
135 FSRVAR 140

RESULT 15
US-10-282-122A-54956
; Sequence 54956, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54956
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54956

Query Match 100.0%; Score 31; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
135 FSRVAR 140

RESULT 16
US-10-437-963-176098
; Sequence 176098, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176098
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73880C.1.pep
US-10-437-963-176098

Query Match 100.0%; Score 31; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
117 FSRVAR 122

RESULT 17
US-10-369-493-23258
; Sequence 23258, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23258
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23258

Query Match 100.0%; Score 31; DB 4; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
76 FSRVAR 81

RESULT 18
US-11-087-099-1759
; Sequence 1759, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 1759
LENGTH: 463
TYPE: PRT
ORGANISM: Bacillus subtilis subsp. subtilis str. 168
US-11-087-099-1759

Query Match 100.0%; Score 31; DB 6; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||||
Db 76 FSRYPAR 81

RESULT 19
US-11-188-298-12707
Sequence 12707, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 12707
LENGTH: 463
TYPE: PRT
ORGANISM: Bacillus subtilis subsp. subtilis str. 168
US-11-188-298-12707

Query Match 100.0%; Score 31; DB 6; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||||
Db 76 FSRYPAR 81

RESULT 20
US-09-815-242-10270
Sequence 10270, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10270
LENGTH: 474
TYPE: PRT
ORGANISM: Escherichia coli
US-09-815-242-10270

Query Match 100.0%; Score 31; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||||
Db 157 FSRYPAR 162

RESULT 21
US-10-369-493-23518
Sequence 23518, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23518
LENGTH: 474
TYPE: PRT
ORGANISM: Escherichia coli
US-10-369-493-23518

Query Match 100.0%; Score 31; DB 4; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYPAR 6
|||||
Db 157 FSRYPAR 162

RESULT 22
US-10-450-763-54803
Sequence 54803, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 54803
LENGTH: 1225
TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (72)..(120)
; OTHER INFORMATION: Tetrahydrofolate dehydrogenase/cyclohydrolase proteins domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00766C, p-value=1.000e-
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (7)..(211)
; OTHER INFORMATION: Tetrahydrofolate dehydrogenase/cyclohydrolase domain identified by
; OTHER INFORMATION: Pfam, accession name THF_DHG_CYH, E-value=1.1e-134, Pfam score of
; OTHER INFORMATION: 460.9
US-10-450-763-54803

Query Match          100.0%; Score 31; DB 5; Length 1225;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db       613 FSRVAR 618

RESULT 23
US-10-450-763-55178
; Sequence 55178, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 55178
; LENGTH: 1258
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (332)..(380)
; OTHER INFORMATION: Tetrahydrofolate dehydrogenase/cyclohydrolase proteins domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00766C, p-value=1.000e-
; OTHER INFORMATION: 40, raw score of 25.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (267)..(471)
; OTHER INFORMATION: Tetrahydrofolate dehydrogenase/cyclohydrolase domain identified by
; OTHER INFORMATION: Pfam, accession name THF_DHG_CYH, E-value=2.9e-134, Pfam score of
; OTHER INFORMATION: 459.5
US-10-450-763-55178

Query Match          100.0%; Score 31; DB 5; Length 1258;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db       1199 FSRVAR 1204

RESULT 24
US-10-424-599-186222
; Sequence 186222, Application US/10424599
; Publication No. US20040031072A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186222
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(67)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139171C.1.pcp
US-10-424-599-186222

Query Match          90.3%; Score 28; DB 4; Length 67;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db       41 FSRVAR 46

RESULT 25
US-10-424-599-146582
; Sequence 146582, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146582
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103383C.1.pcp
US-10-424-599-146582

Query Match          90.3%; Score 28; DB 4; Length 79;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db       17 FSRVAR 22

RESULT 26
US-10-424-599-265564
; Sequence 265564, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
```

```

: TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53223)B
: CURRENT APPLICATION NUMBER: US/10/424,599
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 285684
: SEQ ID NO 265564
: LENGTH: 85
: TYPE: PRT
: ORGANISM: Glycine max
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(85)
: OTHER INFORMATION: unsure at all Xaa locations
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT847_81824C.1.pep
: US-10-424-599-265564

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Query Match	90.3%	Score 28;	DB 4;	Length 85;
Best Local Similarity	83.3%	Pred. No	1.5e+02;	
Matches	5;	Conservative	1;	Mismatches 0; Gaps 0;

Qy	1	FSRYAR	6
		:	
Db	3	FSKYAR	8

RESULT 27
US-10-183-687-178
; Sequence 178, Application US/10183687
; Publication No. US20030204870A1
GENERAL INFORMATION.

```

1  APPLICANT: Allen, Steve
2  APPLICANT: Allen, William B.
3  APPLICANT: Cahoon, Rebecca
4  APPLICANT: Ebelbaum, Sabine
5  APPLICANT: Famodu, Omolayo O.
6  APPLICANT: Harvell, Leslie T.
7  APPLICANT: Jones, Todd
8  APPLICANT: Kinney, Tony
9  APPLICANT: Klein, Ted
10 APPLICANT: Li, Changliang
11 APPLICANT: Oliveira, Igor Cunha
12 APPLICANT: Sakai, Hajime
13 APPLICANT: Shen, Bo
14 APPLICANT: Tarczyński, Mitchell C.
15 TITLE OF INVENTION: Alteration Of Oil Traits In Plants
16 FILE REFERENCE: B81458 US NA
17 CURRENT APPLICATION NUMBER: 60/301,913
18 CURRENT FILING DATE: 2002-06-27
19 PRIOR APPLICATION NUMBER: 60/301,913
20 PRIOR FILING DATE: 2001-06-29
21 NUMBER OF SEQ ID NOS: 532
22 SOFTWARE: Microsoft Office 97
23 SEQ ID NO 178
24 LENGTH: 90
25 TYPE: PRT
26 ORGANISM: Oryza sativa
27 FEATURE:
28 NAME/KEY: UNSURE
29 LOCATION: (80)
30 OTHER INFORMATION: Xaa = any amino acid
31 FEATURE:
32 NAME/KEY: UNSURE
33 LOCATION: (85)
34 OTHER INFORMATION: Xaa = any amino acid
35 US-10-163-687-178

```

Query Match	90.3%	Score	28	DB	4	Length	90
Best Local	Similarity	83.3%	Pred.	No.	1.5e+02		
Matches	5	Conservative	1	Mismatches	0	Indels	0
						Gaps	0

QY 1 FSRYAR 6

Db 12 FSKYAR 17

```

RESULT 28
US-10-425-115-219020
: Sequence 219020, Application US/10425115
: Publication No. US20040214272A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(53222)B
: CURRENT APPLICATION NUMBER: US/10/425.115
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 369326
: SEQ ID NO 219020
: LENGTH: 91
: TYPE: PRT
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: MRT4577_131339C.1.pep
US-10-425-115-219020

```

Query Match	90.3%	Score 28;	DB 4;	Length 91;
Best Local Similarity	83.3%	Pred. No. 1.ee+02;		
Matches	5;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0

QY	1	FSRYAR	6
Db	72	FSRYSR	77

```

RESULT 29
US-10-767-701-51064
; Sequence 51064, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(51535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 51064
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3480-055-P1-K1-H11.dep
US-10-767-701-51064

```

Query Match	90.3%	Score 28	DB 4	length 123
Best Local Similarity	83.3%	Pred. No.	2.1e+02	
Matches	5	Conservative	1	Mismatches 0; Indels 0; Gaps 0

Qy	1	FSRYAR	6
		:	
Db	3	FSRYAK	8

RESULT 30
US-10-767-701-43382
; Sequence 43382, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.

```
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 43382
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SOBBI-28MAY03-C25332_1.pep
US-10-767-701-43382

Query Match          90.3%; Score 28; DB 4; Length 124;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRYAR 6
        ||:|||
Db      43 FSKYAR 48

RESULT 31
US-10-183-687-174
/ Sequence 174, Application US/10183687
/ Publication No. US20030204870A1
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Allen, William B.
/ APPLICANT: Cahoon, Rebecca
/ APPLICANT: Epebaum, Sabine
/ APPLICANT: Famodu, Omolayo O.
/ APPLICANT: Harwell, Leslie T.
/ APPLICANT: Jones, Todd
/ APPLICANT: Kinney, Tony
/ APPLICANT: Klein, Ted
/ APPLICANT: Li, Changjiang
/ APPLICANT: Oliveira, Igor Cunha
/ APPLICANT: Sakai, Hajime
/ APPLICANT: Shen, Bo
/ APPLICANT: Tarczynski, Mitchell C.
/ TITLE OF INVENTION: Alteration Of Oil Traits In Plants
/ FILE REFERENCE: BBI458 US NA
/ CURRENT APPLICATION NUMBER: US/10/183,687
/ CURRENT FILING DATE: 2002-06-27
/ PRIOR APPLICATION NUMBER: 60/301,913
/ PRIOR FILING DATE: 2001-06-29
/ NUMBER OF SEQ ID NOS: 532
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 174
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (91)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (102)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (116)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (120)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
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/ NAME/KEY: UNSURE
/ LOCATION: (122)
/ OTHER INFORMATION: Xaa = any amino acid
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (125)
/ OTHER INFORMATION: Xaa = any amino acid
US-10-183-687-174

Query Match          90.3%; Score 28; DB 4; Length 132;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRYAR 6
        ||:|||
Db      73 FSKYAR 78

RESULT 32
US-10-501-282-478
/ Sequence 478, Application US/10501282
/ Publication No. US20050203280A1
/ GENERAL INFORMATION:
/ APPLICANT: MCMITCHELL, JOHN CALHOUN
/ APPLICANT: ZAGORSKY, ROBERT JOHN
/ APPLICANT: RUSSELL, DAVID PARRISH
/ APPLICANT: FLETCHER, LEAH DIANE
/ TITLE OF INVENTION: ALLOILOCOCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
/ FILE REFERENCE: AM100780 L2
/ CURRENT APPLICATION NUMBER: US/10/501,282
/ CURRENT FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: 60/333,777
/ PRIOR FILING DATE: 2001-11-29
/ PRIOR APPLICATION NUMBER: 60/426,742
/ PRIOR FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: PCT/US02/36123
/ PRIOR FILING DATE: 2002-11-25
/ NUMBER OF SEQ ID NOS: 6653
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 478
/ LENGTH: 145
/ TYPE: PRT
/ ORGANISM: Alloiococcus otitidis
US-10-501-282-478

Query Match          90.3%; Score 28; DB 5; Length 145;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FSRYAR 6
        ||:|||
Db      122 FSRYSR 127

RESULT 33
US-10-501-282-480
/ Sequence 480, Application US/10501282
/ Publication No. US20050203280A1
/ GENERAL INFORMATION:
/ APPLICANT: MCMITCHELL, JOHN CALHOUN
/ APPLICANT: ZAGORSKY, ROBERT JOHN
/ APPLICANT: RUSSELL, DAVID PARRISH
/ APPLICANT: FLETCHER, LEAH DIANE
/ TITLE OF INVENTION: ALLOILOCOCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
/ FILE REFERENCE: AM100780 L2
/ CURRENT APPLICATION NUMBER: US/10/501,282
/ CURRENT FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: 60/333,777
/ PRIOR FILING DATE: 2001-11-29
/ PRIOR APPLICATION NUMBER: 60/426,742
/ PRIOR FILING DATE: 2002-11-18
```

; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 480
; LENGTH: 172
; TYPE: PRT
; ORGANISM: *Alloicoccus oiticidis*
US-10-501-282-480

Query Match 90.3%; Score 28; DB 5; Length 172;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
|||:
Db 149 FSRYSR 154

RESULT 34
US-09-984-245-156
; Sequence 156, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 174
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-09-984-245-156

Query Match 90.3%; Score 28; DB 3; Length 174;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRYAR 6
|||:
Db 69 FARYAR 74

RESULT 35
US-09-966-262-156
; Sequence 156, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30

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; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 156
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-156
```

```

Query Match          90.3%; Score 28; DB 3; Length 174;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FSRVAR 6
        |||||
Db      69 FARVAR 74
```

```

RESULT 36
US-09-983-966-156
; Sequence 156, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
```

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; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 156
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-156
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```

Query Match          90.3%; Score 28; DB 3; Length 174;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 FSRVAR 6
        |||||
Db      69 FARVAR 74
```

```

RESULT 37
US-10-059-395-156
; Sequence 156, Application US/10059395
; Publication No. US20030018180A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/059,395
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/966,262
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
```



```
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-195-156
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```
Query Match          90.3%; Score 28; DB 4; Length 174;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 FSRYAR 6
        |:||||
Db      69 FARYAR 74
```

```
RESULT 38
US-10-143-090-156
; Sequence 156, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-090-156
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```
Query Match          90.3%; Score 28; DB 4; Length 174;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 FSRYAR 6
        |:||||
Db      69 FARYAR 74
```

```
RESULT 39
US-10-960-251-156
; Sequence 156, Application US/10960251
; Publication No. US20050089911A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1C3
; CURRENT APPLICATION NUMBER: US/10/960,251
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 10/143,090
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,188
; PRIOR FILING DATE: 1997-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-960-251-156
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Query Match          90.3%; Score 28; DB 5; Length 174;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 FSRYAR 6
        |:||||
Db      69 FARYAR 74
```

```
RESULT 40
US-10-437-963-197182
; Sequence 197182, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197182
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
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OTHER INFORMATION: Clone ID: PAT_MRT4530_92964C.1.pep
US-10-437-963-197182

Query Match 90.3%; Score 28; DB 4; Length 179;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
||:||||
Db 10 FARVAR 15

RESULT 41
US-11-096-568A-9600

Sequence 9600, Application US/11096568A
Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nikolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 9600

LENGTH: 225

TYPE: PRT

ORGANISM: Triticum aestivum

NAME/KEY: misc_feature

LOCATION: (1)..(225)

OTHER INFORMATION: Ceres Seq. ID no. 12614812

US-11-096-568A-9600

Query Match 90.3%; Score 28; DB 6; Length 225;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
||:||||
Db 144 FSKVAR 149

RESULT 42
US-10-425-115-314441

Sequence 314441, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 314441

LENGTH: 234

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_4982C.1.pep

US-10-425-115-314441

Query Match 90.3%; Score 28; DB 4; Length 234;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
||:||||
Db 153 FSKVAR 158

RESULT 43
US-10-424-599-254640

Sequence 254640, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 254640

LENGTH: 239

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_71963C.1.pep

US-10-424-599-254640

Query Match 90.3%; Score 28; DB 4; Length 239;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
||:||||
Db 157 FSKVAR 162

RESULT 44
US-10-987-454-122

Sequence 122, Application US/10987454
Publication No. US20050172359A1

GENERAL INFORMATION:

APPLICANT: Moloney, Maurice

APPLICANT: Reid, Alexandra

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLOPORTEINS IN TRANSGENIC

FILE REFERENCE: 9369-311

CURRENT APPLICATION NUMBER: US/10/987,454

CURRENT FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: US 60/519,606

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: US 60/579,733

PRIOR FILING DATE: 2004-06-16

NUMBER OF SEQ ID NOS: 251

SOFTWARE: PatentIn version 3.3

SEQ ID NO 122

LENGTH: 243

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-10-987-454-122

Query Match 90.3%; Score 28; DB 5; Length 243;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
||:||||
Db 159 FSKVAR 164

RESULT 45
US-10-183-687-160

Sequence 160, Application US/10183687
Publication No. US20030204870A1

GENERAL INFORMATION:

APPLICANT: Allen, Steve

APPLICANT: Allen, William B.
APPLICANT: Cahoon, Rebecca
APPLICANT: Epelbaum, Sabine
APPLICANT: Famodu, Omolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Jones, Todd
APPLICANT: Kinney, Tony
APPLICANT: Klein, Ted
APPLICANT: Li, Changjiang
APPLICANT: Oliveira, Igor Cunha
APPLICANT: Sakai, Hajime
APPLICANT: Shen, Bo
APPLICANT: Tarczyński, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BB1458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 160
LENGTH: 244
TYPE: PRT
ORGANISM: Zea mays
US-10-183-687-160

Query Match 90.3%; Score 28; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
||:||||
Db 163 FSKYAR 168

RESULT 46
US-10-425-114-54567
; Sequence 54567, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54567
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700838356_Flt.pep
US-10-425-114-54567

Query Match 90.3%; Score 28; DB 4; Length 256;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
||:||||
Db 174 FSKYAR 179

RESULT 47
US-10-437-963-133297
; Sequence 133297, Application US/10437963

Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133297
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35181C.1.pep
US-10-437-963-133297

Query Match 90.3%; Score 28; DB 4; Length 285;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSRVAR 6
||:||||
Db 204 FSKYAR 209

RESULT 48
US-10-987-454-127
; Sequence 127, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF ABOLIPROTEINS IN TRANSGENIC
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-10-987-454-127

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 128, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice

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; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
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OM protein - protein search, using sw model

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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17	27	87.1	290	6	US-10-953-349-9130
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22	27	87.1	353	6	US-10-953-349-21499
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163	24	77.4	401	7	US-11-056-355B-11254	Sequence 11254, A	236	23	74.2	157	7	US-11-330-403-5576	Sequence 5576, Ap
164	24	77.4	405	7	US-11-056-355B-43248	Sequence 43248, A	237	23	74.2	162	6	US-10-449-902-45762	Sequence 45762, A
165	24	77.4	407	7	US-11-056-355B-74635	Sequence 74635, A	238	23	74.2	174	7	US-11-056-355B-51906	Sequence 51906, A
166	24	77.4	410	7	US-11-330-403-13856	Sequence 13856, A	239	23	74.2	178	7	US-10-953-349-44007	Sequence 44007, A
167	24	77.4	431	6	US-10-449-902-51817	Sequence 51817, A	240	23	74.2	181	6	US-10-953-349-30541	Sequence 30541, A
168	24	77.4	439	6	US-10-370-959-64	Sequence 64, Appl	241	23	74.2	181	7	US-11-056-355B-61218	Sequence 61218, A
169	24	77.4	465	7	US-11-051-725-129	Sequence 129, App	242	23	74.2	184	6	US-10-553-436-335	Sequence 335, App
170	24	77.4	485	7	US-11-051-725-154	Sequence 154, App	243	23	74.2	198	6	US-10-449-902-29036	Sequence 29036, A
171	24	77.4	485	7	US-11-051-725-170	Sequence 170, App	244	23	74.2	201	6	US-10-449-902-88412	Sequence 88412, A

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247	23	74.2	217	7	US-11-330-403-3089	Sequence 3089, Ap
248	23	74.2	217	7	US-11-330-403-9378	Sequence 9378, Ap
249	23	74.2	230	7	US-11-056-355B-69587	Sequence 69587, A
250	23	74.2	233	7	US-11-056-355B-80960	Sequence 80960, A
251	23	74.2	236	7	US-11-056-355B-44005	Sequence 44005, A
252	23	74.2	239	6	US-10-953-349-30540	Sequence 30540, A
253	23	74.2	239	6	US-11-056-355B-61217	Sequence 61217, A
254	23	74.2	241	6	US-10-953-349-20142	Sequence 20142, A
255	23	74.2	242	7	US-11-056-355B-83932	Sequence 83932, A
256	23	74.2	244	6	US-10-953-349-30539	Sequence 30539, A
257	23	74.2	244	7	US-11-056-355B-61216	Sequence 61216, A
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259	23	74.2	250	6	US-10-449-902-53359	Sequence 53359, A
260	23	74.2	251	7	US-11-251-208-433	Sequence 433, App
261	23	74.2	264	6	US-10-953-349-20141	Sequence 20141, A
262	23	74.2	265	7	US-11-056-355B-62734	Sequence 62734, A
263	23	74.2	270	7	US-11-249-111-73	Sequence 73, Appl
264	23	74.2	270	7	US-11-330-403-15694	Sequence 15694, A
265	23	74.2	275	6	US-10-953-349-17802	Sequence 17802, A
266	23	74.2	275	7	US-11-056-355B-54203	Sequence 54203, A
267	23	74.2	280	7	US-11-056-355B-83931	Sequence 83931, A
268	23	74.2	282	7	US-11-056-355B-71608	Sequence 71608, A
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272	23	74.2	301	6	US-10-449-902-30034	Sequence 30034, A
273	23	74.2	301	7	US-11-330-403-4508	Sequence 4508, Ap
274	23	74.2	322	6	US-10-953-349-17801	Sequence 17801, A
275	23	74.2	322	7	US-11-056-355B-54202	Sequence 54202, A
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277	23	74.2	324	6	US-10-449-902-49734	Sequence 49734, A
278	23	74.2	324	7	US-11-174-307B-3318	Sequence 3318, Ap
279	23	74.2	326	7	US-11-330-403-7617	Sequence 7617, Ap
280	23	74.2	330	6	US-10-449-902-51597	Sequence 51597, A
281	23	74.2	335	6	US-10-449-902-56163	Sequence 56163, A
282	23	74.2	341	7	US-11-174-307B-3548	Sequence 3548, Ap
283	23	74.2	341	7	US-11-330-403-16154	Sequence 16154, A
284	23	74.2	343	6	US-10-953-349-17800	Sequence 17800, A
285	23	74.2	343	7	US-11-056-355B-54201	Sequence 54201, A
286	23	74.2	349	7	US-11-056-355B-57436	Sequence 57436, A
287	23	74.2	349	7	US-11-056-355B-62733	Sequence 62733, A
288	23	74.2	352	7	US-11-056-355B-8677	Sequence 8677, Ap
289	23	74.2	353	6	US-10-953-349-35828	Sequence 35828, A
290	23	74.2	354	6	US-10-449-902-35334	Sequence 35334, A
291	23	74.2	354	6	US-10-374-780A-444	Sequence 444, App
292	23	74.2	360	6	US-10-449-902-36594	Sequence 36594, A
293	23	74.2	364	6	US-10-543-046-1	Sequence 1, Appl1
294	23	74.2	367	6	US-10-953-349-7459	Sequence 7459, Ap
295	23	74.2	368	7	US-11-330-403-5008	Sequence 5008, Ap
296	23	74.2	368	7	US-11-330-403-10185	Sequence 10185, A
297	23	74.2	369	7	US-11-056-355B-11607	Sequence 71607, A
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305	23	74.2	386	7	US-11-056-355B-16815	Sequence 16815, A
306	23	74.2	391	7	US-11-223-945-38	Sequence 38, Appl
307	23	74.2	394	6	US-10-953-349-9751	Sequence 9751, Ap
308	23	74.2	395	7	US-11-056-355B-9813	Sequence 9813, Ap
309	23	74.2	397	7	US-11-330-403-10174	Sequence 10174, A
310	23	74.2	397	7	US-11-056-355B-57435	Sequence 57435, A
311	23	74.2	397	7	US-11-330-403-18032	Sequence 18032, A
312	23	74.2	405	7	US-11-056-355B-85402	Sequence 45402, A
313	23	74.2	411	6	US-10-530-187-202	Sequence 202, App
314	23	74.2	413	6	US-10-449-902-48807	Sequence 48807, A
315	23	74.2	418	6	US-10-449-902-55989	Sequence 55989, A
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318	23	74.2	428	7	US-11-056-355B-42312	Sequence 42312, A
319	23	74.2	428	7	US-11-056-355B-89166	Sequence 89166, A
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325	23	74.2	438	7	US-11-056-355B-42311	Sequence 42311, A
326	23	74.2	438	7	US-11-056-355B-89165	Sequence 89165, A
327	23	74.2	438	7	US-11-056-355B-92921	Sequence 92921, A
328	23	74.2	439	7	US-11-056-355B-6673	Sequence 6673, Ap
329	23	74.2	443	7	US-11-056-355B-16814	Sequence 16814, A
330	23	74.2	443	7	US-11-056-355B-6672	Sequence 6672, Ap
331	23	74.2	443	7	US-11-056-355B-16813	Sequence 16813, A
332	23	74.2	445	7	US-11-056-355B-9811	Sequence 9811, Ap
333	23	74.2	451	7	US-11-056-355B-24479	Sequence 24479, A
334	23	74.2	451	7	US-11-056-355B-76635	Sequence 76635, A
335	23	74.2	451	7	US-11-056-355B-80330	Sequence 80330, A
336	23	74.2	451	7	US-11-056-355B-89158	Sequence 89158, A
337	23	74.2	454	7	US-11-056-355B-92914	Sequence 92914, A
338	23	74.2	454	7	US-11-056-355B-42310	Sequence 42310, A
339	23	74.2	454	7	US-11-056-355B-89164	Sequence 89164, A
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345	23	74.2	458	7	US-11-330-403-13700	Sequence 13700, A
346	23	74.2	459	6	US-10-449-902-58879	Sequence 58879, A
347	23	74.2	459	6	US-10-449-902-56696	Sequence 56696, A
348	23	74.2	461	6	US-10-449-902-33487	Sequence 33487, A
349	23	74.2	461	6	US-10-449-902-49645	Sequence 49645, A
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352	23	74.2	461	7	US-11-056-355B-80329	Sequence 80329, A
353	23	74.2	461	7	US-11-056-355B-89157	Sequence 89157, A
354	23	74.2	461	7	US-11-056-355B-92913	Sequence 92913, A
355	23	74.2	461	7	US-11-056-355B-49445	Sequence 4945, Ap
356	23	74.2	463	7	US-11-056-355B-55446	Sequence 55446, A
357	23	74.2	464	6	US-10-449-902-47902	Sequence 47902, A
358	23	74.2	464	6	US-11-330-403-3890	Sequence 3890, Ap
359	23	74.2	465	7	US-11-330-403-13730	Sequence 13390, A
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362	23	74.2	479	7	US-11-056-355B-24477	Sequence 24477, A
363	23	74.2	479	7	US-11-056-355B-55445	Sequence 55445, A
364	23	74.2	483	7	US-11-056-355B-55444	Sequence 55444, A
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368	23	74.2	496	6	US-11-293-697-3264	Sequence 3264, Ap
369	23	74.2	499	7	US-11-056-355B-4944	Sequence 4944, Ap
370	23	74.2	505	7	US-11-056-355B-45401	Sequence 45401, A
371	23	74.2	509	7	US-10-449-902-16414	Sequence 16414, A
372	23	74.2	521	6	US-10-449-902-45440	Sequence 45400, A
373	23	74.2	533	6	US-11-056-355B-17703	Sequence 17703, A
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376	23	74.2	539	7	US-11-330-403-13702	Sequence 13702, A
377	23	74.2	540	6	US-10-449-902-45440	Sequence 45400, A
378	23	74.2	540	6	US-11-056-355B-45440	Sequence 45400, A
379	23	74.2	550	6	US-10-538-066-757	Sequence 757, App
380	23	74.2	550	7	US-11-330-403-13266	Sequence 13266, A
381	23	74.2	553	6	US-10-449-902-43397	Sequence 43397, A
382	23	74.2	565	7	US-11-330-403-16668	Sequence 16668, A
383	23	74.2	575	6	US-10-511-937-2625	Sequence 2625, Ap
384	23	74.2	576	6	US-10-449-902-32695	Sequence 32695, A
385	23	74.2	579	7	US-11-056-355B-17702	Sequence 17702, A
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387	23	74.2	597	7	US-11-311-778-16	Sequence 16, Appl
388	23	74.2	620	6	US-10-511-937-2959	Sequence 2959, Ap
389	23	74.2	626	6	US-10-953-349-7804	Sequence 7804, Ap
390	23	74.2	631	7	US-11-330-403-18087	Sequence 18087, A

391	23	74.2	652	6	US-10-953-349-7803	Sequence 7803, Ap
392	23	74.2	699	6	US-10-196-749-138	Sequence 138, App
393	23	74.2	699	7	US-11-258-349-2	Sequence 2, Appli
394	23	74.2	711	6	US-10-449-902-45958	Sequence 45958, A
395	23	74.2	718	6	US-10-449-902-44584	Sequence 44584, A
396	23	74.2	742	7	US-11-330-403-1215	Sequence 10215, A
397	23	74.2	783	7	US-11-330-403-4599	Sequence 4599, Ap
398	23	74.2	815	6	US-10-553-436-183	Sequence 183, App
399	23	74.2	818	6	US-10-449-902-51784	Sequence 51784, A
400	23	74.2	875	6	US-10-471-571A-4802	Sequence 4802, Ap
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402	23	74.2	952	7	US-11-221-332-86	Sequence 86, Appl
403	23	74.2	1007	7	US-11-273-537-5	Sequence 5, Appli
404	23	74.2	1217	6	US-10-553-436-160	Sequence 180, App
405	23	74.2	1255	6	US-10-538-066-364	Sequence 364, App
406	23	74.2	1255	7	US-11-223-945-43	Sequence 43, Appl
407	23	74.2	1255	7	US-11-105-233-130	Sequence 190, App
408	23	74.2	1255	7	US-11-323-049-9	Sequence 9, Appli
409	23	74.2	1255	7	US-11-323-964-9	Sequence 9, Appli
410	23	74.2	1255	7	US-11-406-679-6	Sequence 6, Appli
411	23	74.2	1255	7	US-11-223-945-40	Sequence 40, Appl
412	23	74.2	1273	7	US-11-056-355B-96451	Sequence 96451, A
413	23	74.2	1308	7	US-11-248-122-2	Sequence 2, Appli
414	23	74.2	1308	7	US-11-248-986-15	Sequence 15, Appl
415	23	74.2	1312	7	US-11-056-355B-66450	Sequence 96450, A
416	23	74.2	1323	6	US-10-530-187-289	Sequence 289, App
417	23	74.2	1325	6	US-10-530-187-288	Sequence 288, App
418	23	74.2	1327	7	US-11-221-333-48	Sequence 48, Appl
419	23	74.2	1330	7	US-11-056-355B-66449	Sequence 96449, A
420	23	74.2	1375	6	US-10-553-436-181	Sequence 181, App
421	23	74.2	1433	7	US-11-056-355B-85575	Sequence 85575, A
422	23	74.2	1439	7	US-11-056-355B-85574	Sequence 85574, A
423	23	74.2	1444	7	US-11-070-573-10	Sequence 10, Appl
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425	23	74.2	1533	7	US-11-330-403-9385	Sequence 9285, Ap
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427	22	71.0	9	7	US-11-253-176-133	Sequence 133, App
428	22	71.0	10	6	US-10-542-508-4	Sequence 4, Appli
429	22	71.0	23	7	US-11-251-734-11	Sequence 11, Appl
430	22	71.0	48	7	US-11-368-086-73	Sequence 73, Appl
431	22	71.0	52	7	US-11-115-024-57	Sequence 57, Appl
432	22	71.0	52	7	US-11-115-024-321	Sequence 321, App
433	22	71.0	58	7	US-11-253-176-10	Sequence 10, Appl
434	22	71.0	58	7	US-11-253-176-20	Sequence 20, Appl
435	22	71.0	58	7	US-11-253-176-24	Sequence 24, Appl
436	22	71.0	62	7	US-11-056-355B-85452	Sequence 85452, A
437	22	71.0	72	6	US-10-953-349-30730	Sequence 30730, A
438	22	71.0	72	7	US-11-056-355B-61292	Sequence 61292, A
439	22	71.0	78	6	US-10-524-434-594	Sequence 594, App
440	22	71.0	79	7	US-11-056-355B-3854	Sequence 3854, Ap
441	22	71.0	86	6	US-10-449-902-36450	Sequence 36450, A
442	22	71.0	86	6	US-10-953-349-4392	Sequence 4392, Ap
443	22	71.0	91	6	US-10-449-902-34501	Sequence 34501, A
444	22	71.0	95	6	US-10-489-071-25	Sequence 25, Appl
445	22	71.0	103	6	US-10-449-902-36190	Sequence 36190, A
446	22	71.0	105	6	US-10-471-571A-4930	Sequence 4930, Ap
447	22	71.0	108	6	US-10-449-902-46934	Sequence 46934, A
448	22	71.0	111	7	US-11-330-123-60	Sequence 60, Appl
449	22	71.0	114	7	US-11-293-697-3998	Sequence 3998, Ap
450	22	71.0	114	7	US-11-056-355B-34934	Sequence 34934, A
451	22	71.0	114	7	US-11-056-355B-51981	Sequence 51981, A
452	22	71.0	114	7	US-11-056-355B-88046	Sequence 88046, A
453	22	71.0	116	7	US-11-183-814-7	Sequence 7, Appli
454	22	71.0	118	6	US-10-471-571A-4412	Sequence 4412, Ap
455	22	71.0	118	7	US-11-140-450-9	Sequence 9, Appli
456	22	71.0	118	7	US-11-330-403-9062	Sequence 9062, Ap
457	22	71.0	119	6	US-10-542-682-12	Sequence 12, Appl
458	22	71.0	119	6	US-10-542-682-13	Sequence 13, Appl
459	22	71.0	119	7	US-11-290-249-7	Sequence 7, Appli
460	22	71.0	121	7	US-11-254-679-26	Sequence 26, Appl
461	22	71.0	121	7	US-11-183-814-13	Sequence 13, Appl
462	22	71.0	124	7	US-11-211-917-50	Sequence 50, Appl
463	22	71.0	124	7	US-11-211-917-96	Sequence 96, Appl

464	22	71.0	124	7	US-11-140-450-7	Sequence 7, Appli
465	22	71.0	124	7	US-11-140-450-8	Sequence 8, Appli
466	22	71.0	124	7	US-11-330-403-11308	Sequence 11308, A
467	22	71.0	130	6	US-10-471-571A-45612	Sequence 45612, A
468	22	71.0	131	6	US-10-449-902-32618	Sequence 32618, A
469	22	71.0	134	7	US-11-293-687-3462	Sequence 3462, Ap
470	22	71.0	138	7	US-11-056-355B-34933	Sequence 34933, A
471	22	71.0	138	7	US-11-056-355B-88045	Sequence 88045, A
472	22	71.0	138	7	US-11-056-355B-107948	Sequence 107948, A
473	22	71.0	138	7	US-11-056-355B-119187	Sequence 119187, A
474	22	71.0	139	6	US-10-953-349-62277	Sequence 62277, A
475	22	71.0	139	7	US-11-056-355B-51980	Sequence 51980, A
476	22	71.0	139	7	US-11-056-355B-68125	Sequence 68125, A
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478	22	71.0	141	6	US-10-449-902-34217	Sequence 34217, A
479	22	71.0	144	7	US-11-056-355B-11833	Sequence 11833, A
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481	22	71.0	145	6	US-10-953-349-34570	Sequence 34570, A
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483	22	71.0	145	7	US-11-056-355B-15650	Sequence 15650, A
484	22	71.0	147	7	US-11-056-355B-107947	Sequence 107947, A
485	22	71.0	147	7	US-11-056-355B-119186	Sequence 119186, A
486	22	71.0	149	6	US-10-953-349-15605	Sequence 15605, A
487	22	71.0	149	6	US-10-953-349-34569	Sequence 34569, A
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489	22	71.0	149	6	US-10-449-902-29990	Sequence 29990, A
490	22	71.0	149	7	US-11-056-355B-6616	Sequence 6616, Ap
491	22	71.0	149	7	US-11-056-355B-57736	Sequence 57736, A
492	22	71.0	153	6	US-10-953-349-6549	Sequence 6549, A
493	22	71.0	164	7	US-11-330-403-12576	Sequence 12576, A
494	22	71.0	165	6	US-10-953-349-33595	Sequence 33595, A
495	22	71.0	165	6	US-10-449-902-36380	Sequence 36380, A
496	22	71.0	165	7	US-11-056-355B-15649	Sequence 15649, A
497	22	71.0	166	7	US-11-056-355B-11832	Sequence 11832, A
498	22	71.0	167	7	US-11-056-355B-52838	Sequence 52838, A
499	22	71.0	168	7	US-11-056-355B-4942	Sequence 4942, Ap
500	22	71.0	169	7	US-11-056-355B-34932	Sequence 34932, A

ALIGNMENTS

RESULT 1

US-11-105-233-53

Sequence 53, Application US/1105233

Publication No. US20060134653A1

GENERAL INFORMATION:

APPLICANT: Thiagalingam et al

TITLE OF INVENTION: Differential Expression of Genes in MSI Tumors

FILE REFERENCE: 1657/2001

CURRENT APPLICATION NUMBER: US/11/105,233

CURRENT FILING DATE: 2005-04-13

NUMBER OF SEQ ID NOS: 202

SOFTWARE: FaSTSeq For Windows Version 4.0

SEQ ID NO 53

LENGTH: 174

TYPE: PRT

ORGANISM: Homo sapiens

US-11-105-233-53

Query Match

Best Local Similarity 90.3%; Score 28; DB 7; Length 174;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSRYAR 6

Db 69 FARYAR 74

RESULT 2

US-11-056-355B-66811

Sequence 66811, Application US/11056355B


```
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 68811
; LENGTH: 225
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(225)
; OTHER INFORMATION: Ceres Seq. ID no. 12614812
US-11-056-355B-68811
```

```
Query Match          90.3%; Score 28; DB 7; Length 225;
Best Local Similarity 83.3%; Pred.No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FSRYAR 6
        ||:||||
Db       144 FSKYAR 149
```

```
RESULT 3
US-11-056-355B-106575
; Sequence 106575, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 106575
; LENGTH: 240
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 13619980
US-11-056-355B-106575
```

```
Query Match          90.3%; Score 28; DB 7; Length 240;
Best Local Similarity 83.3%; Pred.No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FSRYAR 6
        ||:||||
Db       156 FSKYAR 161
```

```
RESULT 4
US-11-056-355B-117814
; Sequence 117814, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
```

```
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117814
; LENGTH: 240
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 13619980
US-11-056-355B-117814
```

```
Query Match          90.3%; Score 28; DB 7; Length 240;
Best Local Similarity 83.3%; Pred.No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FSRYAR 6
        ||:||||
Db       156 FSKYAR 161
```

```
RESULT 5
US-11-056-355B-106574
; Sequence 106574, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 106574
; LENGTH: 243
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(243)
; OTHER INFORMATION: Ceres Seq. ID no. 13619979
US-11-056-355B-106574
```

```
Query Match          90.3%; Score 28; DB 7; Length 243;
Best Local Similarity 83.3%; Pred.No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FSRYAR 6
        ||:||||
Db       159 FSKYAR 164
```

```
RESULT 6
US-11-056-355B-117813
; Sequence 117813, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
```

```
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117813
; LENGTH: 243
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(243)
; OTHER INFORMATION: Ceres Seq. ID no. 13619979
US-11-056-355B-117813

Query Match
Best Local Similarity 90.3%; Score 28; DB 7; Length 243;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 159 FSKVAR 164

RESULT 7
US-11-056-355B-106573
; Sequence 106573, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 106573
; LENGTH: 255
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(255)
; OTHER INFORMATION: Ceres Seq. ID no. 13619978
US-11-056-355B-106573

Query Match
Best Local Similarity 90.3%; Score 28; DB 7; Length 255;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 171 FSKVAR 176

RESULT 8
US-11-056-355B-117812
; Sequence 117812, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117812
; LENGTH: 255
; TYPE: prt
```

```
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(255)
; OTHER INFORMATION: Ceres Seq. ID no. 13619978
US-11-056-355B-117812

Query Match
Best Local Similarity 90.3%; Score 28; DB 7; Length 255;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 171 FSKVAR 176

RESULT 9
US-11-056-355B-68810
; Sequence 68810, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 68810
; LENGTH: 301
; TYPE: prt
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(301)
; OTHER INFORMATION: Ceres Seq. ID no. 12614811
US-11-056-355B-68810

Query Match
Best Local Similarity 90.3%; Score 28; DB 7; Length 301;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRVAR 6
Db 220 FSKVAR 225

RESULT 10
US-11-056-355B-68809
; Sequence 68809, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 68809
; LENGTH: 348
; TYPE: prt
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(348)
; OTHER INFORMATION: Ceres Seq. ID no. 12614810
```

US-11-056-355B-68809

Query Match 90.3% Score 28; DB 7; Length 348;
Best Local Similarity 83.3% Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
|||
Db 267 FSKYAR 272

RESULT 11

US-10-449-902-37988
; Sequence 37988, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37988
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37988

Query Match 90.3% Score 28; DB 6; Length 538;
Best Local Similarity 83.3% Pred. No. 86;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
|||
Db 297 FARYAR 302

RESULT 12

US-10-953-349-9971
; Sequence 9971, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9971
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9971

Query Match 87.1% Score 27; DB 6; Length 129;
Best Local Similarity 83.3% Pred. No. 35;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
|||
Db 31 FSRYGR 36

RESULT 13

US-10-953-349-7495
; Sequence 7495, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7495
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7495

Query Match 87.1% Score 27; DB 6; Length 208;
Best Local Similarity 83.3% Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
|||
Db 126 FSRYVR 131

RESULT 14

US-10-953-349-2963
; Sequence 2963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2963
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2963

Query Match 87.1% Score 27; DB 6; Length 209;
Best Local Similarity 83.3% Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
|||
Db 128 FSRYVR 133

RESULT 15

US-10-953-349-2962
; Sequence 2962, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2962
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-2962

Query Match 87.1%; Score 27; DB 6; Length 216;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVAR 6
|||
Db 135 FSRYVR 140

RESULT 16
US-10-953-349-7494
; Sequence 7494, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7494
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7494

Query Match 87.1%; Score 27; DB 6; Length 222;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVAR 6
|||
Db 140 FSRYVR 145

RESULT 17
US-10-953-349-9130
; Sequence 9130, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9130
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9130

Query Match 87.1%; Score 27; DB 6; Length 290;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVAR 6
|||
Db 31 FSRYVR 36

RESULT 18
US-11-174-307B-202
; Sequence 202, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai

; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 202
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: RRM_1; Pfam Description: RNA recognition motif.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: zf-CCHC; Pfam Description: Zinc knuckle
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 11346381; NR Description: splicing factor-like
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 9843663; NR Description: splicing factor RS233
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 42571091; NR Description: splicing factor RS233
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 34895952; NR Description: putative splicing
; OTHER INFORMATION: factor-like protein [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gl|15528625|dbj|BAB64646.1| putative splicing factor-like protei
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 62650252; NR Description: PREDICTED: similar to
US-11-174-307B-202

Query Match 87.1%; Score 27; DB 7; Length 312;
Best Local Similarity 83.3%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSRVAR 6
|||
Db 59 FSRYVR 64

RESULT 19
US-10-449-902-56777
; Sequence 56777, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 56777
LENGTH: 323
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-56777

Query Match Best Local Similarity 87.1%; Score 27; DB 6; Length 323;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
Db 31 FSRYGR 36

RESULT 20

US-10-953-349-21500
Sequence 21500, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 21500
LENGTH: 334
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21500

Query Match Best Local Similarity 87.1%; Score 27; DB 6; Length 334;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
Db 57 FSRYGR 62

RESULT 21

US-10-449-902-34829
Sequence 34829, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 34829
LENGTH: 338
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-34829

Query Match Best Local Similarity 87.1%; Score 27; DB 6; Length 338;

Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
Db 38 FSRYGR 43

RESULT 22

US-10-953-349-21499
Sequence 21499, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 21499
LENGTH: 353
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21499

Query Match Best Local Similarity 87.1%; Score 27; DB 6; Length 353;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
Db 76 FSRYGR 81

RESULT 23

US-10-449-902-33374
Sequence 33374, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 33374
LENGTH: 374
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-33374

Query Match Best Local Similarity 87.1%; Score 27; DB 6; Length 374;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FSRYAR 6
Db 345 FSRYGR 350

RESULT 24

US-10-449-902-45028
Sequence 45028, Application US/10449902

```
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A0205Y1-US
/ CURRENT APPLICATION NUMBER: US/10/449,902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 45028
/ LENGTH: 374
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-449-902-45028

Query Match      87.1% Score 27; DB 6; Length 374;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      345 FQRYAR 350

RESULT 25
US-10-953-349-21498
/ Sequence 21498, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 21498
/ LENGTH: 464
/ TYPE: PRT
/ ORGANISM: Glycine max
US-10-953-349-21498

Query Match      87.1% Score 27; DB 6; Length 464;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      187 FQRYAR 192

RESULT 26
US-11-330-403-7004
/ Sequence 7004, Application US/11330403
/ Publication No. US20060159563A1
/ GENERAL INFORMATION:
/ APPLICANT: Abad, Mark S.
/ TITLE OF INVENTION: Genes and Uses for Plant Improvement
/ FILE REFERENCE: 38-21(53629)B
/ CURRENT APPLICATION NUMBER: US/11/330,403
/ CURRENT FILING DATE: 2006-01-12
/ NUMBER OF SEQ ID NOS: 19250
/ SEQ ID NO: 7004
/ LENGTH: 478
/ TYPE: PRT
```

```
/ ORGANISM: Caulobacter crescentus CB15
US-11-330-403-7004

Query Match      87.1% Score 27; DB 7; Length 478;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      423 FQRYAR 428

RESULT 27
US-11-399-675-7
/ Sequence 7, Application US/11399675
/ Publication No. US20060179513A1
/ GENERAL INFORMATION:
/ APPLICANT: Sticklen, Masomeh B
/ APPLICANT: Magbool, Shahina B
/ APPLICANT: Dale, Bruce E
/ TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULOSE WHICH
/ FILE REFERENCE: MSU 4.1-814
/ CURRENT APPLICATION NUMBER: US/11/399,675
/ CURRENT FILING DATE: 2006-04-06
/ PRIOR APPLICATION NUMBER: US 60/242,408
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: US 09/981,900
/ PRIOR FILING DATE: 2001-10-18
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 7
/ LENGTH: 488
/ TYPE: PRT
/ ORGANISM: Actinomyces naeslundii
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (113)..(113)
/ OTHER INFORMATION: The 'Xaa' at location 113 stands for leu.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (148)..(148)
/ OTHER INFORMATION: The 'Xaa' at location 148 stands for asp, Gly, Ala, or Val.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (316)..(316)
/ OTHER INFORMATION: The 'Xaa' at location 316 stands for Tyr, Cys, Ser, or Phe.
US-11-399-675-7

Query Match      87.1% Score 27; DB 7; Length 488;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
Db      159 FQRYAR 164

RESULT 28
US-11-353-390A-7
/ Sequence 7, Application US/11353390A
/ Publication No. US20060185036A1
/ GENERAL INFORMATION:
/ APPLICANT: Sticklen, Masomeh B
/ APPLICANT: Magbool, Shahina B
/ APPLICANT: Dale, Bruce E
/ TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULOSE WHICH
/ FILE REFERENCE: MSU 4.1-806
/ CURRENT APPLICATION NUMBER: US/11/353,390A
/ CURRENT FILING DATE: 2006-02-14
/ PRIOR APPLICATION NUMBER: US 60/242,408
/ PRIOR FILING DATE: 2000-10-20
```

```

; PRIOR APPLICATION NUMBER: US 09/981,900
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Actinomyces naeslundii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (113)..(113)
; OTHER INFORMATION: The 'Xaa' at location 113 stands for Leu.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: The 'Xaa' at location 148 stands for Asp, Gly, Ala, or Val.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (316)..(316)
; OTHER INFORMATION: The 'Xaa' at location 316 stands for Tyr, Cys, Ser, or Phe.
US-11-353-390A-7

Query Match      87.1%; Score 27; DB 7; Length 488;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 FSRVAR 6
        |||||
Db      159 FERYAR 164
```

```

RESULT 29
US-11-354-310A-7
; Sequence 7, Application US/11354310A
; Publication No. US20060185037A1
; GENERAL INFORMATION:
; APPLICANT: Sticklen, Masomeh B
; APPLICANT: Magbool, Shahina B
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULOSE WHICH
; FILE REFERENCE: MSU 4.1-805
; CURRENT APPLICATION NUMBER: US/11/354,310A
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: US 60/242,408
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/981,900
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Actinomyces naeslundii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (113)..(113)
; OTHER INFORMATION: The 'Xaa' at location 113 stands for Leu.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: The 'Xaa' at location 148 stands for Asp, Gly, Ala, or Val.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (316)..(316)
; OTHER INFORMATION: The 'Xaa' at location 316 stands for Tyr, Cys, Ser, or Phe.
US-11-354-310A-7
```

```

Query Match      87.1%; Score 27; DB 7; Length 488;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 FSRVAR 6
```

```
Db      159 FERYAR 164
        |||||
```

```

RESULT 30
US-11-174-307B-4272
; Sequence 4272, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4272
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: ABC1; Pfam Description: ABC1 family
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50935257; NR Description: ABC1 family protein
; OTHER INFORMATION: kinase-like protein [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|23617237|dbj|BAC20904.1| ABC1 family protein kinase-like
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 24215277; NR Description: ABC1 family protein
; OTHER INFORMATION: protein [Leptospira interrogans serovar Lai str. 56601]
; OTHER INFORMATION: >gi|24196371|gb|AA49776.1| ABC1 family protein kinase [Leptospira
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 45657281; NR Description: ubiquinone biosynthesis
; OTHER INFORMATION: protein [Leptospira interrogans serovar Copenhagen str. Fliocruz
; OTHER INFORMATION: >gi|39574567|emb|CAE78409.1| Gene product involved in ubiquinone
US-11-174-307B-4272
```

```

Query Match      87.1%; Score 27; DB 7; Length 541;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 FSRVAR 6
        |||||
Db      50 FSRVAR 55
```

```

RESULT 31
US-10-449-902-33781
; Sequence 33781, Application US/10449902
```

```
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33781
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33781

Query Match      83.9%; Score 26; DB 6; Length 107;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRVAR 6
        |||||
        88 FSRVAR 93
DB

RESULT 32
US-11-056-355B-581
; Sequence 581, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 581
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(109)
; OTHER INFORMATION: Ceres Seq. ID no. 13635683
US-11-056-355B-581

Query Match      83.9%; Score 26; DB 7; Length 109;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmut, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
; FILE REFERENCE: 0091 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/337,300
; CURRENT FILING DATE: 2006-01-20
; NUMBER OF SEQ ID NOS: 478
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 451
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Variable heavy chain of SC03-057
US-11-337-300-451

Query Match      83.9%; Score 26; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSRYA 5
        |||||
        31 FSRYA 35
DB

RESULT 34
US-10-449-902-31883
; Sequence 31883, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31883
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31883

Query Match      83.9%; Score 26; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FSRVAR 6
        |||||
        49 FSRVAR 54
DB

RESULT 33
US-11-337-300-451
; Sequence 451, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruijf, Cornelis A.
```

```
US-11-056-355B-16531
; Sequence 16531, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
```



```

; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 16531
; LENGTH: 219
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(219)
; OTHER INFORMATION: Ceres Seq. ID no. 12352826
US-11-056-355B-16531

Query Match
Best Local Similarity 83.9%; Score 26; DB 7; Length 219;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYA 5
Db 13 FSRYA 17

RESULT 36
US-11-056-355B-16851
; Sequence 16851, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 16851
; LENGTH: 219
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(219)
; OTHER INFORMATION: Ceres Seq. ID no. 12566294
US-11-056-355B-16851

Query Match
Best Local Similarity 83.9%; Score 26; DB 7; Length 219;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYA 5
Db 13 FSRYA 17

RESULT 37
US-11-337-300-286
; Sequence 286, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Krulff, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
; FILE REFERENCE: 0091 WO 00 00D
; CURRENT APPLICATION NUMBER: US/11/337,300
; CURRENT FILING DATE: 2006-01-20
; NUMBER OF SEQ ID NOS: 478
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 256
; TYPE: prt
```

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SC03-057
US-11-337-300-286

Query Match
Best Local Similarity 83.9%; Score 26; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYA 5
Db 32 FSRYA 36

RESULT 38
US-10-449-902-30299
; Sequence 30299, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30299
; LENGTH: 271
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-30299

Query Match
Best Local Similarity 83.9%; Score 26; DB 6; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSRYA 5
Db 65 FSRYA 69

RESULT 39
US-10-449-902-31725
; Sequence 31725, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31725
; LENGTH: 271
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-31725
```

Query Match 83.9%; Score 26; DB 6; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVA 5
 |||||
 Db 65 FSRVA 69

RESULT 40
 US-10-449-902-32135
 ; Sequence 32135, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A02051-US
 ; CURRENT APPLICATION NUMBER: US/10/449, 902
 ; PRIOR FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32135
 ; LENGTH: 271
 ; TYPE: prt
 ; ORGANISM: Oryza sativa
 US-10-449-902-32135

Query Match 83.9%; Score 26; DB 6; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVA 5
 |||||
 Db 65 FSRVA 69

RESULT 41
 US-10-449-902-51604
 ; Sequence 51604, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A02051-US
 ; CURRENT APPLICATION NUMBER: US/10/449, 902
 ; PRIOR FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 51604
 ; LENGTH: 271
 ; TYPE: prt
 ; ORGANISM: Oryza sativa
 US-10-449-902-51604

Query Match 83.9%; Score 26; DB 6; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVA 5

Db 65 FSRVA 69
 |||||

RESULT 42
 US-11-056-355B-7374
 ; Sequence 7374, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056, 355B
 ; PRIOR FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 7374
 ; LENGTH: 271
 ; TYPE: prt
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(271)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12412613
 US-11-056-355B-7374

Query Match 83.9%; Score 26; DB 7; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVA 5
 |||||
 Db 65 FSRVA 69

RESULT 43
 US-11-056-355B-16849
 ; Sequence 16849, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056, 355B
 ; PRIOR FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 16849
 ; LENGTH: 271
 ; TYPE: prt
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(271)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12566292
 US-11-056-355B-16849

Query Match 83.9%; Score 26; DB 7; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVA 5
 |||||
 Db 65 FSRVA 69

RESULT 44

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US-11-056-355B-7372
; Sequence 7372, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2/50-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7372
; LENGTH: 311
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(311)
; OTHER INFORMATION: Ceres Seq. ID no. 12412611
US-11-056-355B-7372

Query Match          83.9%; Score 26; DB 7; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 FSRVYR 5
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Db      105 FSRVYR 109

RESULT 45
US-11-330-403-9151
; Sequence 9151, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 9151
; LENGTH: 334
; TYPE: prt
; ORGANISM: Staphylococcus aureus subsp. aureus Mu50
US-11-330-403-9151

Query Match          83.9%; Score 26; DB 7; Length 334;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 FSRVYR 6
        |||||
Db      103 FSEVYR 108

RESULT 46
US-11-330-403-19189
; Sequence 19189, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 19189
; LENGTH: 334
; TYPE: prt
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; ORGANISM: Staphylococcus aureus subsp. aureus MW2
US-11-330-403-19189

Query Match          83.9%; Score 26; DB 7; Length 334;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 FSRVYR 6
        |||||
Db      103 FSEVYR 108

RESULT 47
US-11-404-745-2
; Sequence 2, Application US/11404745
; Publication No. US20060179505A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL
; TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAP1) GENE DISRUPTIONS
; FILE REFERENCE: R-490
; CURRENT APPLICATION NUMBER: US/11/404,745
; CURRENT FILING DATE: 2006-04-14
; PRIOR APPLICATION NUMBER: US/10/109,616
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,509
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/311,055
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: prt
; ORGANISM: Mus musculus
US-11-404-745-2

Query Match          83.9%; Score 26; DB 7; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 FSRVYR 6
        |||||
Db      146 FSRVYR 151

RESULT 48
US-11-359-554-3
; Sequence 3, Application US/11359554
; Publication No. US20060154293A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Prostatein-Like
; TITLE OF INVENTION: Serine Protease
; FILE REFERENCE: 004974.00929
; CURRENT APPLICATION NUMBER: US/11/359,554
; CURRENT FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: US/10/311,591
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US 60/213,474
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/277,612
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-359-554-3

Query Match          83.9%; Score 26; DB 7; Length 343;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRVAR 6
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 Db 146 FSRVAR 151

Search completed: August 29, 2006, 11:29:12
 Job time : 4.75248 secs

RESULT 49
 US-10-471-571A-4440
 ; Sequence 4440, Application US/10471571A
 ; Publication No. US20060115490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE: P026927WO
 ; CURRENT APPLICATION NUMBER: US/10/471,571A
 ; CURRENT FILING DATE: 2003-09-12
 ; PRIOR APPLICATION NUMBER: GB-0107661.1
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 5642
 ; SOFTWARE: Seqwin99, version 1.03
 ; SEQ ID NO 4440
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(348)
 ; OTHER INFORMATION: conserved hypothetical
 US-10-471-571A-4440

Query Match 83.9%; Score 26; DB 6; Length 348;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FSRVAR 6
 |||||
 Db 117 FSRVAR 122

RESULT 50
 US-11-333-747A-22
 ; Sequence 22, Application US/11333747A
 ; Publication No. US20060160159A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Handfield, Martin
 ; APPLICANT: Hillman, Jeffrey
 ; APPLICANT: Proguiske-Fox, Ann
 ; TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans
 ; TITLE OF INVENTION: Antigens for use in the diagnosis, treatment, and monitoring
 ; FILE REFERENCE: MBHB01-662C
 ; CURRENT APPLICATION NUMBER: US/11/333,747A
 ; CURRENT FILING DATE: 2006-01-17
 ; PRIOR APPLICATION NUMBER: US 09/995493
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: PCT/US02/37235
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 234
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 365
 ; TYPE: PRT
 ; ORGANISM: Actinobacillus actinomycetemcomitans
 US-11-333-747A-22

Query Match 83.9%; Score 26; DB 7; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSRVA 5
 |||||
 Db 278 FSRVA 282

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 05:46:47 ; Search time 45.7426 Seconds
(without alignments)
69.968 Million cell updates/sec

Title: US-10-541-343-3

Perfect score: 38

Sequence: 1 WMLSAFS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

1: A_Geneseq.8:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	7	ADQ90197	Adq90197 WMLSAFS d
2	38	100.0	13	ADQ90200	Adq90200 MNTF 13 m
3	38	100.0	33	AAW59046	Aaw59046 Human MNT
4	38	100.0	33	AAO29914	Aao29914 Human mot
5	38	100.0	33	ADQ90195	Adq90195 MNTF1-F6
6	35	92.1	1760	ABBS3367	Abbs3367 Drosophila
7	35	92.1	1760	ABG70020	Abg70020 Larval v1
8	33	86.8	17	ADX56419	Adx56419 Cardiov
9	33	86.8	35	AAAS29781	Aaas29781 Human MSF
10	33	86.8	61	AAAB4007	Aaab4007 Human can
11	33	86.8	538	AAO18834	Aao18834 3' cartil
12	33	86.8	902	AAAB29778	Aab29778 Human MSF
13	33	86.8	933	ADQ67713	Adq67713 Novel hum
14	33	86.8	981	ADZ03664	Adz03664 PRG4-Lub
15	33	86.8	1007	ADZ03668	Adz03668 PRG4-Lub
16	33	86.8	1038	ADZ03672	Adz03672 PRG4-Lub
17	33	86.8	1069	ADZ03676	Adz03676 PRG4-Lub
18	33	86.8	1100	ADZ03680	Adz03680 PRG4-Lub
19	33	86.8	1270	ADK67911	Adk67911 Human ext
20	33	86.8	1299	AAW24322	Aaw24322 Human EST
21	33	86.8	1311	ADK67912	Adk67912 Human ext
22	33	86.8	1320	ADK65819	Adk65819 Angiogene
23	33	86.8	1404	AAK26049	Aak26049 MSF precu

24	33	86.8	1404	AAAB29773	Aab29773 Human meg
25	33	86.8	1404	AAAB60568	Aab60568 Human meg
26	33	86.8	1404	ADK65839	Adk65839 Angiogene
27	33	86.8	1404	ADM98014	Adm98014 Human meg
28	33	86.8	1404	ADK69335	Adk69335 Human meg
29	33	86.8	1404	ADY15658	Ady15658 PRO polyp
30	33	86.8	1404	AED66477	Aed66477 Human lub
31	33	86.8	1404	AEP54256	Aep54256 Megakaryo
32	33	86.8	1404	AEP89839	Aep89839 Human meg
33	33	86.8	1415	AAU32262	Aau32262 Novel hum
34	32	84.2	31	AAAB82730	Aab82730 Human imm
35	32	84.2	81	ABP04103	Abp04103 Human ORF
36	32	84.2	103	ADC95262	Adc95262 E. faeciu
37	32	84.2	211	AAU25590	Aau25590 Human G p
38	32	84.2	243	ADRO9699	Adro9699 Human pro
39	32	84.2	262	ABO73613	Ab073613 Pseudomon
40	32	84.2	280	AAAG1234	Aaag1234 Mycobacte
41	32	84.2	289	AAAM51647	Aaam51647 Human GPC
42	32	84.2	289	ADQ29555	Adq29555 Mouse GPC
43	32	84.2	289	ADQ29554	Adq29554 Human GPC
44	32	84.2	323	AAU25612	Aau25612 Human G p
45	32	84.2	323	ABBO6257	Abbo6257 Human G p
46	32	84.2	371	ABJ10905	Abj10905 Human, sec
47	32	84.2	437	ABO60886	Ab060886 Klebsiell
48	32	84.2	561	ADF70484	Adf70484 Orphan re
49	32	84.2	1180	ADU02401	Adu02401 Novel hum
50	32	84.2	1923	ABG21342	Abg21342 Novel hum
51	31	81.6	13	AAAB23728	Aab23728 Phaneoroch
52	31	81.6	76	AAAM94607	Aam94607 Human rep
53	31	81.6	76	ADB09815	Abd09815 Alilolcoc
54	31	81.6	91	ABP52882	Abp52882 Human imm
55	31	81.6	93	AAAM85209	Aam85209 Human imm
56	31	81.6	146	AAAB54191	Aab54191 Human pan
57	31	81.6	193	AGS30491	Ag30491 Arabidops
58	31	81.6	199	ADU17777	Adu17777 Reverse t
59	31	81.6	204	AAAG30490	Ag30490 Arabidops
60	31	81.6	229	AAAG6722	Ag6722 Arabidops
61	31	81.6	229	AAAG45332	Ag45332 Arabidops
62	31	81.6	263	AAU82738	Aau82738 Amino ac
63	31	81.6	265	AAAG30489	Ag30489 Arabidops
64	31	81.6	290	AAAG6721	Ag6721 Arabidops
65	31	81.6	290	AAAG45331	Ag45331 Arabidops
66	31	81.6	299	AAAG45330	Ag45330 Arabidops
67	31	81.6	299	AAAG6720	Ag6720 Arabidops
68	31	81.6	299	ADN74439	Adn74439 Thale cre
69	31	81.6	305	ADX74105	Adx74105 Plant ful
70	31	81.6	362	AAAP81100	Aap81100 Sequence
71	31	81.6	362	ABB70453	Abb70453 Drosophi
72	31	81.6	371	AAU79553	Aau79553 P. chryso
73	31	81.6	397	ADZ13153	Adz13153 Human can
74	30	78.9	50	ABO55588	Ab055588 Human gen
75	30	78.9	117	ADX40178	Adx40178 HIV Rev p
76	30	78.9	119	ADCC94073	Adc94073 E. faeciu
77	30	78.9	152	ABO14240	Ab014240 Novel hum
78	30	78.9	152	ADG78647	Adg78647 Human sec
79	30	78.9	152	ADN60938	Adn60938 Human sec
80	30	78.9	155	ADBO9737	Adbo9737 Alilolcoc
81	30	78.9	158	AAAG72847	Aag72847 Human oif
82	30	78.9	174	ADAS7140	Ada57140 Human sec
83	30	78.9	174	ADAA1004	Ada41004 Human sec
84	30	78.9	174	ABO14025	Ab014025 Novel hum
85	30	78.9	174	ADD37949	Add37949 Human sec
86	30	78.9	174	ADG78431	Adg78431 Human sec
87	30	78.9	174	ADN60722	Adn60722 Human sec
88	30	78.9	175	AAAG72846	Aag72846 Human oif
89	30	78.9	176	AAAG72845	Aag72845 Human oif
90	30	78.9	182	ADN23223	Adn23223 Bacteri
91	30	78.9	191	ADC95755	Adc95755 E. faeciu
92	30	78.9	230	ABO81807	Ab081807 Pseudomon
93	30	78.9	244	ABE81722	Ab81722 L. pneumo
94	30	78.9	246	AEBS8464	Aeb38464 L. pneumo
95	30	78.9	273	ADN20738	Adn20738 Bacteri
96	30	78.9	320	ADD93502	Ad93502 Pavlova 1

97	30	78.9	320	9	ADM11906	Adw11906	Pavlova 1	170	29	76.3	335	6	ABU82132	Abu82132	Novel hum
98	30	78.9	320	9	AED95183	Aed95183	Pavlova 1	171	29	76.3	335	6	ABU72312	Abu72312	Novel hum
99	30	78.9	321	6	ADA36340	Ada36340	Acinetoba	172	29	76.3	335	6	ABO33618	AbO33618	Novel hum
100	30	78.9	332	4	AAB88503	Aab88503	Haemophil	173	29	76.3	335	6	ABJ72440	AbJ72440	Human PRO
101	30	78.9	332	5	AAU91434	Aau91434	Haemophil	174	29	76.3	335	6	ABO34335	AbO34335	Human sec
102	30	78.9	359	7	ABO67049	AbO67049	Klebsiell	175	29	76.3	335	7	ABO44471	AbO44471	Human sec
103	30	78.9	420	6	ABP56696	AbP56696	Human int	176	29	76.3	335	7	ABO33495	AbO33495	Novel hum
104	30	78.9	464	8	ADH39760	AdH39760	Streptomy	177	29	76.3	335	7	ABU72142	AbJ72142	Human mem
105	30	78.9	481	7	ABM90405	AbM90405	Rice abio	178	29	76.3	335	7	ADH83660	AdH83660	Novel hum
106	30	78.9	496	7	ABM66642	AbM66642	Rice abio	179	29	76.3	335	7	ADH80766	AdH80766	Novel hum
107	30	78.9	526	4	AAB93482	Aab93482	Human pro	180	29	76.3	335	7	ADH73307	AdH73307	Novel hum
108	30	78.9	526	4	ABB97533	Abb97533	Novel hum	181	29	76.3	335	7	ADH78389	Adh78389	Novel hum
109	30	78.9	628	7	ABO75995	AbO75995	Pseudomon	182	29	76.3	335	7	ADH85037	Adh85037	Human PRO
110	30	78.9	736	8	ADX68450	Adx68450	Plant ful	183	29	76.3	335	7	ADH78143	Adh78143	Novel hum
111	30	78.9	818	8	ADX71975	Adx71975	Plant ful	184	29	76.3	335	7	ADH87209	Adh87209	Human PRO
112	30	78.9	907	4	ABB62840	Abb62840	Drosophil	185	29	76.3	335	7	ADH84791	Adh84791	Human PRO
113	30	78.9	907	4	ABE44576	AbE44576	Sleep dis	186	29	76.3	335	7	ADH83906	Adh83906	Novel hum
114	30	78.9	1321	8	ADN23423	Adn23423	Bacteri-al	187	29	76.3	335	7	ADH73061	Adh73061	Novel hum
115	30	78.9	1372	8	ADN23424	Adn23424	Bacteri-al	188	29	76.3	335	7	ADH79999	Adh79999	Human PRO
116	30	78.9	2250	9	ADY27516	Ady27516	HCoV-NL63	189	29	76.3	335	7	ADH79999	Adh79999	Human PRO
117	30	78.9	4055	9	AEA06399	Aea06399	EMCR coro	190	29	76.3	335	7	ADH79999	Adh79999	Human PRO
118	30	78.9	4055	9	ADY27513	Ady27513	Amino aci	191	29	76.3	335	7	ADH79999	Adh79999	Human PRO
119	30	78.9	6738	9	ADY27514	Ady27514	Amino aci	192	29	76.3	335	7	ADH79999	Adh79999	Human PRO
120	30	78.9	6738	9	ADY27515	Ady27515	Amino aci	193	29	76.3	335	7	ADH79999	Adh79999	Human PRO
121	29	76.3	58	5	ABP11194	AbP11194	Human ORF	194	29	76.3	335	7	ADH79999	Adh79999	Human PRO
122	29	76.3	60	3	AAB38320	Aab38320	Human sec	195	29	76.3	335	7	ADH79999	Adh79999	Human PRO
123	29	76.3	87	4	AAU17729	Aau17729	Novel hum	196	29	76.3	335	7	ADH79999	Adh79999	Human PRO
124	29	76.3	87	7	ADG41109	Adg41109	Human res	197	29	76.3	335	7	ADH79999	Adh79999	Human PRO
125	29	76.3	87	7	ADP96883	Adp96883	Human res	198	29	76.3	335	7	ADH79999	Adh79999	Human PRO
126	29	76.3	106	5	ABH89390	Abh89390	Human pol	199	29	76.3	335	7	ADH79999	Adh79999	Human PRO
127	29	76.3	113	8	ADH11789	Adh11789	Human sec	200	29	76.3	335	7	ADH79999	Adh79999	Human PRO
128	29	76.3	113	8	ADY06261	Ady06261	Plant ful	201	29	76.3	335	7	ADH79999	Adh79999	Human PRO
129	29	76.3	114	8	AAV76167	Aav76167	Human sec	202	29	76.3	335	7	ADH79999	Adh79999	Human PRO
130	29	76.3	117	8	ADY05513	Ady05513	Plant ful	203	29	76.3	335	7	ADH79999	Adh79999	Human PRO
131	29	76.3	127	2	AAH88723	Aah88723	Secreted	204	29	76.3	335	7	ADH79999	Adh79999	Human PRO
132	29	76.3	127	4	ABH50490	Abh50490	Human sec	205	29	76.3	335	7	ADH79999	Adh79999	Human PRO
133	29	76.3	127	6	ABO44747	AbO44747	Novel hum	206	29	76.3	335	7	ADH79999	Adh79999	Human PRO
134	29	76.3	127	6	ABO26227	AbO26227	Human pro	207	29	76.3	335	7	ADH79999	Adh79999	Human PRO
135	29	76.3	129	5	ABP06040	AbP06040	Human ORF	208	29	76.3	335	7	ADH79999	Adh79999	Human PRO
136	29	76.3	132	4	AAO04045	Aao04045	Human pol	209	29	76.3	335	7	ADH79999	Adh79999	Human PRO
137	29	76.3	146	6	ABU18616	Abu18616	Protein e	210	29	76.3	335	7	ADH79999	Adh79999	Human PRO
138	29	76.3	146	8	ADP59661	Adp59661	Human pol	211	29	76.3	335	7	ADH79999	Adh79999	Human PRO
139	29	76.3	186	8	ADX09022	Adx09022	Plant ful	212	29	76.3	335	7	ADH79999	Adh79999	Human PRO
140	29	76.3	200	4	AAO06824	Aao06824	Human pol	213	29	76.3	335	7	ADH79999	Adh79999	Human PRO
141	29	76.3	218	4	AAH95287	Aah95287	Human pro	214	29	76.3	335	7	ADH79999	Adh79999	Human PRO
142	29	76.3	222	9	ADY65804	Ady65804	S. mansoni	215	29	76.3	335	7	ADH79999	Adh79999	Human PRO
143	29	76.3	238	7	ADP58723	Adp58723	Human pol	216	29	76.3	335	7	ADH79999	Adh79999	Human PRO
144	29	76.3	243	2	AAW55241	Aaw55241	H. pylori	217	29	76.3	335	7	ADH79999	Adh79999	Human PRO
145	29	76.3	250	9	ADM26637	Adm26637	Fructo-col	218	29	76.3	335	7	ADH79999	Adh79999	Human PRO
146	29	76.3	252	8	ADY06260	Ady06260	Plant ful	219	29	76.3	335	7	ADH79999	Adh79999	Human PRO
147	29	76.3	272	2	AAW71530	Aaw71530	Helicobac	220	29	76.3	335	7	ADH79999	Adh79999	Human PRO
148	29	76.3	279	2	AAW55471	Aaw55471	H. pylori	221	29	76.3	335	7	ADH79999	Adh79999	Human PRO
149	29	76.3	293	3	AAW54475	Aaw54475	Arabi-dops	222	29	76.3	335	7	ADH79999	Adh79999	Human PRO
150	29	76.3	293	4	ABG06787	Abg06787	Novel hum	223	29	76.3	335	8	ADH79999	Adh79999	Human PRO
151	29	76.3	295	3	AAW37367	Aaw37367	Pbdl (Wbp	224	29	76.3	335	8	ADH79999	Adh79999	Human PRO
152	29	76.3	303	2	AAW37367	Aaw37367	Pbdl (Wbp	225	29	76.3	335	8	ADH79999	Adh79999	Human PRO
153	29	76.3	304	3	AAW37367	Aaw37367	Pbdl (Wbp	226	29	76.3	335	8	ADH79999	Adh79999	Human PRO
154	29	76.3	306	3	AAW37367	Aaw37367	Pbdl (Wbp	227	29	76.3	335	8	ADH79999	Adh79999	Human PRO
155	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	228	29	76.3	335	8	ADH79999	Adh79999	Human PRO
156	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	229	29	76.3	335	8	ADH79999	Adh79999	Human PRO
157	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	230	29	76.3	335	8	ADH79999	Adh79999	Human PRO
158	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	231	29	76.3	335	8	ADH79999	Adh79999	Human PRO
159	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	232	29	76.3	335	8	ADH79999	Adh79999	Human PRO
160	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	233	29	76.3	335	8	ADH79999	Adh79999	Human PRO
161	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	234	29	76.3	335	8	ADH79999	Adh79999	Human PRO
162	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	235	29	76.3	335	8	ADH79999	Adh79999	Human PRO
163	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	236	29	76.3	335	8	ADH79999	Adh79999	Human PRO
164	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	237	29	76.3	335	8	ADH79999	Adh79999	Human PRO
165	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	238	29	76.3	335	8	ADH79999	Adh79999	Human PRO
166	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	239	29	76.3	335	8	ADH79999	Adh79999	Human PRO
167	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	240	29	76.3	335	8	ADH79999	Adh79999	Human PRO
168	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	241	29	76.3	335	8	ADH79999	Adh79999	Human PRO
169	29	76.3	307	3	AAW37367	Aaw37367	Pbdl (Wbp	242	29	76.3	335	8	ADH79999	Adh79999	Human PRO

243	29	76.3	335	8	ADb85601	Novel hum	316	29	76.3	624	7	ADb60520	Ad660520 Rat Prote
244	29	76.3	335	8	ADb05150	Human PRO	317	29	76.3	624	7	ADb60516	Ad660516 Rat Prote
245	29	76.3	335	8	ADb75363	Human PRO	318	29	76.3	624	7	ADb09403	Adb09403 Human pro
246	29	76.3	335	8	ADb76907	Novel hum	319	29	76.3	689	4	ABG00041	Abg00041 Novel hum
247	29	76.3	335	8	ADb86675	Novel hum	320	29	76.3	722	10	AEF13718	Aef13718 Aphanothe
248	29	76.3	335	8	ADb78143	Novel hum	321	29	76.3	722	9	AEA21035	Aea21035 Novel hum
249	29	76.3	335	8	ADb77651	Novel hum	322	29	76.3	806	5	ABP62885	Abp62885 Human pol
250	29	76.3	335	8	ADb77897	Novel hum	323	29	76.3	806	7	ADJ69027	Adj69027 Human hea
251	29	76.3	335	8	ADb85355	Novel hum	324	29	76.3	806	8	ADb65804	Adb65804 Novel hum
252	29	76.3	335	8	ADb73887	Human PRO	325	29	76.3	810	8	ADQ18928	Adq18928 Human sof
253	29	76.3	335	8	ADb74625	Human PRO	326	29	76.3	845	3	AAQ30758	Aaq30758 Arabidops
254	29	76.3	335	8	ADb77153	Novel hum	327	29	76.3	851	3	AAQ30757	Aaq30757 Arabidops
255	29	76.3	335	8	ADb85847	Novel hum	328	29	76.3	859	3	AAQ30756	Aaq30756 Arabidops
256	29	76.3	335	8	ADb05396	Human PRO	329	29	76.3	895	3	AAQ45341	Aaq45341 Arabidops
257	29	76.3	335	8	ADb74871	Human PRO	330	29	76.3	903	3	AAQ45340	Aaq45340 Arabidops
258	29	76.3	335	8	ADb96503	Human PRO	331	29	76.3	982	3	AAQ45339	Aaq45339 Arabidops
259	29	76.3	335	8	ADb25814	Human sec	332	29	76.3	1065	6	ABU37008	Abu37008 Protein e
260	29	76.3	335	8	ADb24713	Human sec	333	29	76.3	1818	5	ABP73779	Abp73779 Candida a
261	29	76.3	335	8	ADb29449	Human sec	334	29	76.3	1878	4	ABB61852	Abb61852 Drosophi1
262	29	76.3	335	8	ADb96980	Human sec	335	29	76.3	2005	4	ABG24464	Abg24464 Novel hum
263	29	76.3	335	8	ADb05683	Novel hum	336	29	76.3	4101	8	ADN23857	Adn23857 Bacterial
264	29	76.3	335	8	ADb27237	Human PRO	337	29	76.3	4101	8	ADN23856	Adn23856 Bacterial
265	29	76.3	335	8	ADb11300	Novel hum	338	29	76.3	4924	4	AAb70968	Aab70968 S. spinos
266	29	76.3	335	8	ADb12079	Novel hum	339	29	76.3	4928	2	AAV39300	Aav39300 Spnd a po
267	29	76.3	335	8	ADb94636	Novel hum	340	29	76.3	4933	6	ABP57681	Abp57681 Saccharop
268	29	76.3	335	8	ADb06732	Human PRO	341	28	73.7	25	8	ABO54055	Ab054055 Human gen
269	29	76.3	335	8	ADb03018	Human sec	342	28	73.7	52	8	ADb87749	Adb87749 Plant ful
270	29	76.3	335	8	ADb03972	Human sec	343	28	73.7	60	4	AAb37179	Aab37179 Peptide #
271	29	76.3	335	8	ADb03495	Human sec	344	28	73.7	61	4	AAg77571	Aag77571 Human col
272	29	76.3	335	8	ADb39076	Novel hum	345	28	73.7	63	4	ABG08861	Abg08861 Novel hum
273	29	76.3	335	8	ADb43623	Human PRO	346	28	73.7	71	3	AAQ35290	Aaq35290 Zea may5
274	29	76.3	335	8	ADb34166	Novel hum	347	28	73.7	71	3	AAQ35299	Aaq35299 Zea may5
275	29	76.3	335	8	ADb04449	Human sec	348	28	73.7	73	3	AAQ18848	Aaq18848 Zea may5
276	29	76.3	335	8	ADb13636	Human PRO	349	28	73.7	74	3	ABb29829	Abb29829 Human sec
277	29	76.3	335	8	ADb69730	Human PRO	350	28	73.7	75	2	AAW20820	Aaw20820 H. pylori
278	29	76.3	335	8	ADb61450	Human sec	351	28	73.7	75	4	ABb41555	Abb41555 Peptide #
279	29	76.3	335	8	ADb129891	Novel hum	352	28	73.7	75	4	AAb35346	Aab35346 Peptide #
280	29	76.3	335	8	ADb27288	Novel hum	353	28	73.7	75	4	AAW52334	Aaw52334 Human bon
281	29	76.3	335	8	ADb82968	Human PRO	354	28	73.7	75	4	AAb62426	Aab62426 Human bra
282	29	76.3	335	8	ADb66646	Human PRO	355	28	73.7	75	4	ABG56996	Abg56996 Human liv
283	29	76.3	335	8	ADb191857	Human PRO	356	28	73.7	75	5	ABG44887	Abg44887 Human pep
284	29	76.3	335	8	ADb194649	Human sec	357	28	73.7	76	4	AAU45193	Aau45193 Propionib
285	29	76.3	335	8	ADb94363	Human PRO	358	28	73.7	76	4	AAU63295	Aau63295 Propionib
286	29	76.3	335	9	ADb17816	Novel hum	359	28	73.7	76	6	ABb41712	Abb41712 Propionib
287	29	76.3	335	9	ADb63337	Human c10	360	28	73.7	76	6	ABb59814	Abb59814 Propionib
288	29	76.3	335	9	ADb79911	Amtno aci	361	28	73.7	78	4	AAW24468	Aaw24468 Human EST
289	29	76.3	335	9	AEb45036	Human sec	362	28	73.7	80	2	AAV60165	Aav60165 Human end
290	29	76.3	336	6	ABb67175	Photocorb	363	28	73.7	80	6	ABJ18385	Abj18385 Breast sp
291	29	76.3	347	3	AAQ44754	Arabidops	364	28	73.7	82	3	AAQ33806	Aaq33806 Arabidops
292	29	76.3	349	3	AAQ49475	Arabidops	365	28	73.7	89	5	ABb98392	Abb98392 Cytochrom
293	29	76.3	350	3	AAQ32965	Arabidops	366	28	73.7	89	5	ABJ10235	Abj10235 Human lun
294	29	76.3	350	3	AAQ32965	Arabidops	367	28	73.7	93	9	AEb83040	Aeb83040 Hyperimmu
295	29	76.3	356	5	ABb47847	Listeria	368	28	73.7	98	7	ADb15994	Adb15994 G-coupled
296	29	76.3	357	5	ADb75994	Plant pol	369	28	73.7	98	8	ADb19393	Adb19393 Human G-C
297	29	76.3	359	7	ABb79984	Pseudomon	370	28	73.7	100	8	ABb054783	Abb054783 Human gen
298	29	76.3	360	4	AAb00105	Tritosepho	371	28	73.7	103	5	ABb10024	Abb10024 Human pro
299	29	76.3	376	4	ADb65381	Novel hum	372	28	73.7	103	5	ABb10006	Abb10006 Human pro
300	29	76.3	381	3	AAQ32964	Arabidops	373	28	73.7	103	5	ABG64646	Abg64646 Human alb
301	29	76.3	407	8	ADb23095	Plant ful	374	28	73.7	103	5	ABG64647	Abg64647 Human alb
302	29	76.3	414	8	ADb09740	Plant ful	375	28	73.7	103	6	ADb55367	Adb55367 Human pro
303	29	76.3	428	8	ADb09849	Plant ful	376	28	73.7	103	6	ADb57056	Adb57056 Human pro
304	29	76.3	437	5	ADb91891	Agarase I	377	28	73.7	103	6	ADb57460	Adb57460 Human sec
305	29	76.3	445	8	ADb192225	Urokinase	378	28	73.7	103	6	ADb41339	Adb41339 Human sec
306	29	76.3	463	8	ADb135098	Xylanase	379	28	73.7	103	6	ADb440999	Adb440999 Human sec
307	29	76.3	483	5	ABP29825	Streptococ	380	28	73.7	103	6	ABR47825	AbR47825 Human sec
308	29	76.3	483	5	ADb88149	Streptococ	381	28	73.7	103	6	ABR48062	AbR48062 Human sec
309	29	76.3	483	8	ADb79402	Streptococ	382	28	73.7	103	7	ADb74494	Adb74494 Human sec
310	29	76.3	488	9	ADb81578	Streptococ	383	28	73.7	103	7	ADb74214	Adb74214 Human sec
311	29	76.3	488	9	ABb57468	L. acidop	384	28	73.7	103	7	ADb38047	Adb38047 Human sec
312	29	76.3	495	9	ABb57264	L. acidop	385	28	73.7	103	7	ADb37922	Adb37922 Human sec
313	29	76.3	545	8	ADb21402	Bacterial	386	28	73.7	103	8	ADb77913	Adb77913 Albumin f
314	29	76.3	585	8	ADb27112	Bacterial	387	28	73.7	103	8	ADb77914	Adb77914 Albumin f
315	29	76.3	598	8	ADb29798	Bacterial	388	28	73.7	107	3	AAb40942	Aab40942 Human ORF

389	28	73.7	107	5	ABP09313	Abp09313 Human ORF	462	28	73.7	291	8	ADO29637	Ado29637 Mouse GPC
390	28	73.7	108	5	ABP63769	ABP63769 Human ORF	463	28	73.7	294	9	ABE837487	Aeb37487 L. pneumo
391	28	73.7	111	3	AA645463	AA645463 Arabidops	464	28	73.7	294	9	ABE83748	Aeb36748 L. pneumo
392	28	73.7	120	2	AAV12283	AAV12283 Human 5'	465	28	73.7	297	3	AA620022	AA620022 Arabidops
393	28	73.7	124	8	AD126137	AD126137 Human pro	466	28	73.7	297	3	AA654067	AA654067 Arabidops
394	28	73.7	127	3	AAV73436	AAV73436 Human sec	467	28	73.7	302	3	AA618090	AA618090 Arabidops
395	28	73.7	130	3	AA600184	AA600184 Human sec	468	28	73.7	302	3	AA643063	AA643063 Arabidops
396	28	73.7	137	3	AA645462	AA645462 Arabidops	469	28	73.7	304	4	ABG02510	ABG02510 Novel hum
397	28	73.7	141	3	AA628194	AA628194 Arabidops	470	28	73.7	304	10	AEF29059	AEF29059 Lead Cere
398	28	73.7	146	9	ABE41704	ABE41704 L. pneumo	471	28	73.7	305	3	AA630769	AA630769 Arabidops
399	28	73.7	153	9	ABE16602	ABE16602 B. subtil	472	28	73.7	305	5	ABE890870	ABE890870 Herbicida
400	28	73.7	157	7	ADC95874	ADC95874 E. faeciu	473	28	73.7	305	5	ABE84448	ABE84448 Siah-rela
401	28	73.7	161	6	ABM69553	ABM69553 Phototfab	474	28	73.7	305	6	ABP71511	ABP71511 Arabidops
402	28	73.7	162	4	AA698902	AA698902 E. coli G	475	28	73.7	305	8	ADU74828	ADU74828 Arabidops
403	28	73.7	167	8	ADY11547	ADY11547 Plant ful	476	28	73.7	305	8	ADU24241	ADU24241 Arabidops
404	28	73.7	169	8	ADP08496	ADP08496 Plant ful	477	28	73.7	305	9	ADP84931	ADP84931 Arabidops
405	28	73.7	178	8	ADN12271	ADN12271 IL-1R/TLR	478	28	73.7	306	6	ABP71512	ABP71512 Arabidops
406	28	73.7	180	6	ABR43184	ABR43184 Human REM	479	28	73.7	307	3	AA651216	AA651216 Arabidops
407	28	73.7	196	3	AA628193	AA628193 Arabidops	480	28	73.7	307	9	ADP84933	ADP84933 Arabidops
408	28	73.7	198	4	ABG21897	ABG21897 Novel hum	481	28	73.7	308	3	AA654066	AA654066 Arabidops
409	28	73.7	204	8	ADP56658	ADP56658 Human Tol	482	28	73.7	308	3	AA620021	AA620021 Arabidops
410	28	73.7	204	8	ADP48599	ADP48599 Human Tol	483	28	73.7	308	3	AA609499	AA609499 Arabidops
411	28	73.7	211	3	ABE38444	ABE38444 L. pneumo	484	28	73.7	309	3	AAE58153	AAE58153 Lung canc
412	28	73.7	214	3	AA643064	AA643064 Arabidops	485	28	73.7	311	3	AA630559	AA630559 Arabidops
413	28	73.7	214	3	AA618091	AA618091 Arabidops	486	28	73.7	311	5	ABE91960	ABE91960 Herbicida
414	28	73.7	214	4	AA692865	AA692865 C. glutami	487	28	73.7	315	5	ABE84458	ABE84458 Siah-rela
415	28	73.7	214	7	ADL65953	ADL65953 C. glutam	488	28	73.7	317	6	ABP57736	ABP57736 S. pombe
416	28	73.7	214	7	ADL65575	ADL65575 C. glutam	489	28	73.7	317	6	ADP81925	ADP81925 Plant ful
417	28	73.7	214	9	AED72620	AED72620 Coryneb	490	28	73.7	320	8	ADP25091	ADP25091 PRO polyp
418	28	73.7	214	9	AA688060	AA688060 Human Tol	491	28	73.7	321	3	AA643062	AA643062 Arabidops
419	28	73.7	223	3	ABM97246	ABM97246 M. xanthu	492	28	73.7	322	3	AA618089	AA618089 Arabidops
420	28	73.7	230	3	AA628192	AA628192 Arabidops	493	28	73.7	322	7	ABO80187	ABO80187 Pseudomon
421	28	73.7	237	7	ABO70264	ABO70264 Pseudomon	494	28	73.7	322	8	ADP67518	ADP67518 Plant ful
422	28	73.7	242	3	AA630771	AA630771 Arabidops	495	28	73.7	325	3	AA640192	AA640192 Arabidops
423	28	73.7	245	2	AAV42302	AAV42302 Trehalose	496	28	73.7	325	3	AA620782	AA620782 Arabidops
424	28	73.7	246	2	AAV37559	AAV37559 C. tracho	497	28	73.7	326	3	AA651215	AA651215 Arabidops
425	28	73.7	247	6	ADA34361	ADA34361 Acinetoba	498	28	73.7	326	5	ABR47476	ABR47476 Listeria
426	28	73.7	253	9	ADY52914	ADY52914 Nostoc pu	499	28	73.7	326	5	ABU31154	ABU31154 Protein e
427	28	73.7	253	3	ADY52966	ADY52966 Nostoc pu	500	28	73.7	326	6		
428	28	73.7	254	3	AA628191	AA628191 Arabidops							
429	28	73.7	259	4	ABG16894	ABG16894 Novel hum							
430	28	73.7	261	8	ADT57199	ADT57199 Plant pol							
431	28	73.7	267	2	AAW22303	AAW22303 Rat CRTI							
432	28	73.7	267	8	ADL27274	ADL27274 Amino aci							
433	28	73.7	267	8	AED40557	AED40557 Murine XB							
434	28	73.7	268	4	AA644860	AA644860 Heart mus							
435	28	73.7	268	4	AA699931	AA699931 Human Mes							
436	28	73.7	268	5	ABG61851	ABG61851 Prostate							
437	28	73.7	268	9	ABE53855	ABE53855 Prostate							
438	28	73.7	275	4	ABE66537	ABE66537 Drosophi1							
439	28	73.7	279	8	ADS22855	ADS22855 Bacterial							
440	28	73.7	280	8	ADP29737	ADP29737 Human sec							
441	28	73.7	281	3	AA630770	AA630770 Arabidops							
442	28	73.7	288	5	ABE84985	ABE84985 Human PRO							
443	28	73.7	288	5	ABE95591	ABE95591 Human ang							
444	28	73.7	288	5	ADP60852	ADP60852 Human sto							
445	28	73.7	288	7	ADDI0627	ADDI0627 Human sec							
446	28	73.7	288	7	ADDI1587	ADDI1587 Human sec							
447	28	73.7	288	7	ADD37380	ADD37380 Human sec							
448	28	73.7	288	8	ADDE1588	ADDE1588 Human sec							
449	28	73.7	288	8	ADH43771	ADH43771 Human PRO							
450	28	73.7	288	8	ADK83116	ADK83116 Human PRO							
451	28	73.7	288	8	ADN16966	ADN16966 Resistin							
452	28	73.7	288	8	ADN97418	ADN97418 Human sto							
453	28	73.7	288	8	ADY19786	ADY19786 PRO polyp							
454	28	73.7	288	9	ADY14388	ADY14388 PRO polyp							
455	28	73.7	288	9	AE838715	AE838715 L. pneumo							
456	28	73.7	288	9	AE840801	AE840801 L. pneumo							
457	28	73.7	288	9	AE841938	AE841938 L. pneumo							
458	28	73.7	288	9	AE840132	AE840132 L. pneumo							
459	28	73.7	288	9	AA620023	AA620023 Arabidops							
460	28	73.7	290	3	AA654068	AA654068 Arabidops							
461	28	73.7	290	3									

ALIGNMENTS

RESULT 1
 ID ADO90197 standard; peptide; 7 AA.
 AC ADO90197;
 DT 21-OCT-2004 (first entry)
 XX
 DE WMLSAFS domain motoneuronotrophic factor peptide analogue.
 XX
 KW motoneuronotrophic; motor neuron; Noctropic; Neuroprotective; Vulnerary;
 KM Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
 KW peripheral nerve; neurodegenerative; wound healing.
 XX
 OS Unidentified.
 XX
 FN W02004065410-A2.
 PD 05-AUG-2004.
 XX
 PF 21-JAN-2004; 2004WO-US001468.
 XX
 PR 21-JAN-2003; 2003US-0441772P.
 PA (GENE-) GENEVRON BIOPHARMACEUTICALS LLC.
 XX
 PI Chau RMW, Ko TD;
 XX WPI; 2004-562147/54.
 DR

XX New motoneuronotrophic factor peptide analogue enhancing the viability of
 PT motor neurons, useful for target muscle reinnervation, treating
 PT peripheral nerve injuries or neurodegenerative diseases and in wound
 PT healing.
 XX
 PS Claim 1; SEQ ID NO 3; 40pp; English.
 XX
 CC The present invention relates to motoneuronotrophic factor peptide
 CC analogue, where the peptide analogue enhances the viability of motor
 CC neurons. The methods and compositions of the present invention are useful
 CC for promoting motor neuron viability and axon degeneration, target muscle
 CC reinnervation, treating peripheral nerve injuries, treating
 CC neurodegenerative disease and in wound healing. The present sequence
 CC represents WMLSAFS domain motoneuronotrophic factor peptide analogue.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 38; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 WMLSAFS 7
 |||||
 Db 1 WMLSAFS 7
 RESULT 2
 ADQ90200
 ID ADQ90200 standard; peptide; 13 AA.
 XX
 AC ADQ90200;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 XX NMTF 13 mer motoneuronotrophic factor peptide analogue.
 DE
 XX motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnerary;
 KW Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
 KW peripheral nerve; neurodegenerative; wound healing.
 XX
 OS Unidentified.
 OS
 XX WO2004065410-A2.
 PN
 XX 05-AUG-2004.
 PD
 XX 21-JAN-2004; 2004WO-US001468.
 PF
 XX 21-JAN-2003; 2003US-0441772P.
 PR
 XX (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
 PA
 XX Chau RMW, Ko TD;
 PI
 XX WPI; 2004-562147/54.
 DR
 XX New motoneuronotrophic factor peptide analogue enhancing the viability of
 PT motor neurons, useful for target muscle reinnervation, treating
 PT peripheral nerve injuries or neurodegenerative diseases and in wound
 PT healing.
 XX
 PS Claim 7; SEQ ID NO 6; 40pp; English.
 XX
 CC The present invention relates to motoneuronotrophic factor peptide
 CC analogue, where the peptide analogue enhances the viability of motor
 CC neurons. The methods and compositions of the present invention are useful
 CC for promoting motor neuron viability and axon degeneration, target muscle
 CC reinnervation, treating peripheral nerve injuries, treating
 CC neurodegenerative disease and in wound healing. The present sequence
 CC represents a NMTF motoneuronotrophic factor peptide analogue.
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 38; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 WMLSAFS 7
 |||||
 Db 2 WMLSAFS 8
 RESULT 3
 AAM59046
 ID AAM59046 standard; protein; 33 AA.
 XX
 AC AAM59046;
 XX
 DT 11-AUG-1998 (first entry)
 XX
 DE Human NMTF1-F6 protein fragment.
 XX
 KW Motoneuronotrophic factor; NMTF-1; NMTF1-F6; human; axon regeneration;
 KW motoneuron; diagnose; treatment; disease; wound healing; scar tissue;
 KW keloid.
 XX
 OS Homo sapiens.
 OS
 XX WO9813492-A2.
 PN
 XX 02-APR-1998.
 PD
 XX 22-SEP-1997; 97WO-US017142.
 PF
 XX 27-SEP-1996; 96US-0026792P.
 PR 15-NOV-1996; 96US-00751225.
 PR 12-SEP-1997; 97US-00928862.
 XX
 PA (KMBI-) KM BIOTECH INC.
 XX
 PI Chau RMW;
 XX
 DR WPI; 1998-230703/20.
 DR N-PADB; AAV11748.
 DR
 XX Motoneuronotrophic factor NMTF1-F3 and NMTF1-F6 - useful for motoneuron
 PT regeneration, diagnosing or treating motoneuron disease and to accelerate
 PT wound healing without scar formation.
 XX
 PS Claim 4; Fig 2B; 78pp; English.
 XX
 CC This sequence, represents a fragment of a novel human motoneuronotrophic
 CC factor, NMTF1-F6. Such factors are used to promote regeneration of the
 CC axon of a motoneuron, to diagnose and treat motoneuron disease in a
 CC mammal or to accelerate wound healing whilst concomitantly minimizing or
 CC inhibiting scar tissue and/or keloid formation in an area associated with
 CC a wound. For promoting axonal regeneration, the polypeptide is
 CC administered at a concentration of 5 ng-50 mg, whereas for inhibiting
 CC hereditary motoneuron disease, the dosage is 5-100 (especially 30-50)mg
 CC per kg body weight
 CC
 SQ Sequence 33 AA;
 Query Match 100.0%; Score 38; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 WMLSAFS 7
 |||||
 Db 12 WMLSAFS 18
 RESULT 4
 AAO29914
 ID AAO29914 standard; protein; 33 AA.

XX AA029914;
AC 03-SEP-2003 (first entry)
DT
XX
DE Human motoneuronotrophic factor (NMN1F)1-F6 protein.
XX
XX Human; motoneuronotrophic factor; NMN1F; therapy; radiation therapy;
KM peripheral nerve injury; musculoskeletal disorder; spinal cord injury;
KM head injury; stroke; neuromuscular degenerative disease; nootropic;
KM amyotrophic lateral sclerosis; peripheral neuropathy; neuroprotective;
KM muscular dystrophy; AIDS; spinal muscular atrophy; multiple sclerosis;
KM scar; myasthenia gravis; sensory neuronal function disorder; vulnary;
KM cancer.
XX
XX Homo sapiens.
OS
XX WO2003044175-A2.
PN
XX 30-MAY-2003.
PD
XX 19-NOV-2002; 2002WO-US037191.
PF
XX 20-NOV-2001; 2001US-00989481.
PR
XX (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
PA
XX Chau RMW;
PI
XX WPI; 2003-457607/43.
XX
DR N-PSDB; AAL60573.
XX
XX Promoting the survival, growth, proliferation or maintenance of mammalian
PT neurons by administering motoneuronotrophic factors, useful for treating
PT musculoskeletal and neurodegenerative disorders and spinal cord injuries.
XX
XX Claim 1; Fig 2B; 90pp; English.
PS
XX
XX The invention relates to a method for promoting the survival, growth,
CC proliferation or maintenance of mammalian neurons by administering
CC motoneuronotrophic factors (NMN1F). The method is useful for treating
CC peripheral nerve injuries, musculoskeletal disorders, spinal cord
CC injuries, head injuries, strokes, neuromuscular degenerative diseases,
CC amyotrophic lateral sclerosis, spinal muscular atrophy, peripheral
CC neuropathy, diabetic peripheral neuropathy, peripheral neuropathy
CC resulting from AIDS or radiation therapy for cancer, multiple sclerosis,
CC muscular dystrophy, inhibition of scar formation, myasthenia gravis and
CC sensory neuronal function disorders. The present sequence is human NMN1F-
CC F6 protein used to illustrate the method of the invention
XX
XX Sequence 33 AA;
SQ
Query Match 100.0%; Score 38; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
Db 12 WMLSAFS 18
RESULT 5
AD090195
XX AD090195 standard; peptide; 33 AA.
XX
AC AD090195;
XX
DT 21-OCT-2004 (first entry)
XX
DE NMN1F-F6 33 mer motoneuronotrophic factor peptide analogue.
XX
XX motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnary;
KM Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
KM

KM peripheral nerve; neurodegenerative; wound healing.
XX
XX Unidentified.
OS
XX WO2004065410-A2.
PN
XX 05-AUG-2004.
PD
XX 21-JAN-2004; 2004WO-US001468.
PF
XX 21-JAN-2003; 2003US-0441772P.
PR
XX (GENE-) GENERVON BIOPHARMACEUTICALS LLC.
PA
XX Chau RMW, Ko TD;
PI
XX WPI; 2004-562147/54.
DR
XX New motoneuronotrophic factor peptide analogue enhancing the viability of
PT motor neurons, useful for target muscle reinnervation, treating
PT peripheral nerve injuries or neurodegenerative diseases and in wound
PT healing.
XX
XX Claim 2; SEQ ID NO 1; 40pp; English.
PS
XX
XX The present invention relates to motoneuronotrophic factor peptide
CC analogue, where the peptide analogue enhances the viability of motor
CC neurons. The methods and compositions of the present invention are useful
CC for promoting motor neuron viability and axon degeneration, target muscle
CC reinnervation, treating peripheral nerve injuries, treating
CC neurodegenerative disease and in wound healing. The present sequence
CC represents NMN1F-F6 33 mer motoneuronotrophic factor peptide analogue.
XX
XX Sequence 33 AA;
SQ
Query Match 100.0%; Score 38; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
Db 12 WMLSAFS 18
RESULT 6
ABB63367
XX ABB63367 standard; protein; 1760 AA.
ID
AC ABB63367;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 16893.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR

DR N-PSDB; ABL07470.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 16893; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins (AB57737-
CC AB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1760 AA;
XX
Query Match 92.1%; Score 35; DB 4; Length 1760;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 WMLSAFS 7
DB 966 MWVSARS 972
XX
RESULT 7
ABG70020
ID ABG70020 standard; protein; 1760 AA.
XX
AC ABG70020;
XX
DT 05-NOV-2002 (first entry)
XX
DE Larval viability associated protein #19.
XX
XX Fruit fly; larval viability; insecticidal activity; maize; wheat; oat;
XX rye; sorghum; rice; barley; millet; cotton; sugarcane; sugar beet;
XX oilseed rape; soybean; vegetable crop; fruit.
XX
XX Drosophila melanogaster.
XX
XX WO200257455-A2.
XX
XX 25-JUL-2002.
XX
XX 18-JAN-2002; 2002WO-US001568.
XX
XX 18-JAN-2001; 2001US-0262351P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Stam L, Bachmann J, Broadus J, Kamdar KP;
XX
XX WPI; 2002-590746/63.
XX
XX N-PSDB; AB551396.
XX
PT Identifying inhibitors of activity of proteins essential for Drosophila
PT larval viability comprising expressing in a host a protein essential for
PT larval activity and identifying compounds that inhibit or interact with
PT the protein.
XX
XX Claim 1; Page 120-126; 169pp; English.
XX
CC The invention describes a method of identifying compounds that inhibit
CC the activity of, or that interact with a protein essential for Drosophila
CC larval viability comprising expressing in a recombinant host a DNA
CC molecule to produce a protein essential for larval viability. The method
CC is useful for identifying compounds with insecticidal activity. Compounds

CC identified are useful as insecticides in crops such as maize, wheat,
CC oats, rye, sorghum, rice, barley, millet, turf, cotton, sugarcane, sugar
CC beet, oilseed rape, soybeans, vegetable crops and fruits. This is the
CC amino acid sequence of a fruit fly larval viability associated protein
XX
XX Sequence 1760 AA;
XX
Query Match 92.1%; Score 35; DB 5; Length 1760;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 WMLSAFS 7
DB 966 MWVSARS 972
XX
RESULT 8
ADX56419
ID ADX56419 standard; peptide; 17 AA.
XX
XX ADX56419;
XX
AC 05-MAY-2005 (first entry)
XX
DE Cardiovascular disorder plasma protein tryptic fragment SEQ ID NO 236.
XX
XX coronary artery disease; primary biliary cirrhosis; gallstones;
XX celiac disease; irritable bowel syndrome; diabetes; scleroderma; nausea;
XX emesis; constipation; diarrhea; cardiovascular disease; immune disorder;
XX endocrine disease; gastrointestinal disease; metabolic disorder;
XX dermatological disease; musculoskeletal disease; Cardiant; Vasotropic;
XX Hepatotropic; Litholytic; Immunosuppressive; Gastrointestinal.Gen.;
XX Antiinflammatory; Antidiabetic; Dermatological; Antiemetic; Laxative;
XX Antidiarrhetic; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2005015206-A2.
XX
XX 17-FEB-2005.
XX
XX 06-AUG-2004; 2004WO-EP008860.
XX
XX 08-AUG-2003; 2003US-0493599P.
XX
XX 08-AUG-2003; 2003US-0493836P.
XX
XX 08-AUG-2003; 2003US-0493867P.
XX
XX 08-AUG-2003; 2003US-0493985P.
XX
XX (XENO-) XENOVA LTD.
XX
XX (NOVS) NOVARTIS AG.
XX
XX (NOVS) NOVARTIS PHARMA GMBH.
XX
XX Argoud-Puy G, Bedert N, Bougueleret L, Cusin I, Mahe E,
XX Niknejad A, Refas S, Rose K, Saudrais C, Scherer A, Papoian R;
XX
XX WPI; 2005-195824/20.
XX
XX
XX Screening and/or diagnosing cardiovascular disorder in subject involves
XX detecting and/or quantifying level of polypeptide in biological sample
XX from subject and comparing with control sample.
XX
XX Claim 1; SEQ ID NO 236; 349pp; English.
XX
XX The invention relates to a method of screening and/or diagnosing a
XX cardiovascular disorder (CD) in a subject which comprises detecting
XX and/or quantifying the level of a polypeptide in a biological sample from
XX the subject and comparing the level to that of control sample. The method
XX is useful for screening, diagnosing and treating coronary artery disease,
XX biliary cirrhosis, gallstones, celiac disease, irritable bowel syndrome,
XX diabetes, scleroderma, nausea, vomiting, constipation and diarrhea. The
XX method is rapid and efficient. The present sequence represents a
XX cardiovascular disorder plasma protein tryptic fragment.

SQ Sequence 17 AA;

Query Match 86.8%; Score 33; DB 9; Length 17;

Best Local Similarity 85.7%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7

| | | | |

Db 5 WMLSPFS 11

RESULT 9

AAB29781

ID AAB29781 standard; peptide; 35 AA.

AC AAB29781;

DT 28-FEB-2001 (first entry)

DE Human MSF-derived tribonectin fragment #3.

XX Human tribonectin; MSF, megakaryocyte stimulating factor;

KM alternative splicing; joint boundary lubricant; O-linked oligosaccharide;

KM osteoarthritis; tribosupplementator; tissue adhesion inhibition;

KM friction coefficient reduction; gene therapy; antiarthritic; osteopathic.

OS Homo sapiens.

XX WO200064930-A2.

PN 02-NOV-2000.

XX 24-APR-2000; 2000WO-US010953.

XX 23-APR-1999; 99US-00298970.

XX (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.

XX Jay GD;

XX WPI; 2001-024673/03.

XX Novel tribonectin polypeptide useful as lubricant for treating

PT osteoarthritis, comprises O-linked lubricating moiety.

PS Disclosure; Fig 1; 47pp; English.

XX The invention relates to a human tribonectin which is a product of

CC alternative splicing of the human MSF (megakaryocyte stimulating factor)

CC gene. The tribonectin has at least one O-linked oligosaccharide

CC lubricating moiety and has a polypeptide sequence comprising 1-76 repeats

CC of a motif having at least 50% identity to the sequence KEPPPT

CC (AAB29781). The invention also relates to a nucleic acid encoding a human

CC MSF-derived tribonectin; a biocompatible composition comprising a human

CC tribonectin for inhibiting tissue adhesion formation; and a method of

CC diagnosing osteoarthritis or a predisposition to osteoarthritis by

CC measuring the amount of MSF or its fragment in a biological sample of a

CC mammal, wherein an increased amount of MSF compared to a control

CC indicates the presence of or predisposition to developing osteoarthritis.

CC The tribonectin and DNA encoding it are useful in the treatment of

CC osteoarthritis, where they may be used for lubricating mammalian joints,

CC such as articulating joints of humans, dogs or horses. The tribonectin,

CC when formulated as a membrane, foam, gel or fibre, is useful for

CC inhibiting adhesion between two surfaces such as the injured tissues of a

CC mammal, where the injury is caused by a surgical insertion or trauma, or

CC an artificial device e.g., an orthopaedic implant. In particular, one of

CC the surfaces is pericardial tissue. DNA encoding a tribonectin may be

CC used in gene therapy. The present sequence represents a fragment of a

CC human MSF-derived tribonectin

XX Sequence 35 AA;

SQ Query Match 86.8%; Score 33; DB 4; Length 35;

Best Local Similarity 85.7%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7

| | | | |

Db 6 WMLSPFS 12

RESULT 10

AAB44007

ID AAB44007 standard; protein; 61 AA.

AC AAB44007;

DT 08-FEB-2001 (first entry)

DE Human cancer associated protein sequence SEQ ID NO:1452.

XX Human, cancer associated gene; cancer antigen; detection; cancer;

KM diagnosis; cytostatic; proliferative; vulnery; immunomodulator;

KM antidiabetic; antisthmatic; antineumatic; antiarthritic; antiviral;

KM antiinflammatory; antihyroid; antiallergic; antibacterial; cardiac;

KM dermatological; neuroprotective; thrombolytic; coagulant; neotropic;

KM vasotropic; antipruritic; antiangiogenic; gene therapy; inflammatory;

KM immune disorder; haematopoietic cell disorder; autoimmune disorder;

KM allergic reaction; graft versus host disease; organ rejection;

KM haemostatic; thrombolytic; cardiovascular disorder; infection;

KM neurological disease; drug screening.

OS Homo sapiens.

XX WO200055350-A1.

PN 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005882.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

XX N-PSDB; AAC78216.

XX Novel isolated nucleic acids comprising sequences encoding peptides

PT useful for treating or diagnosing e.g. cancer.

PS Claim 11; Page 2133; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in

CC AAB43398 to AAB44239. The proteins can have activities based on the

CC tissues and cells the genes are expressed in. Example of activities

CC include: cytostatic; proliferative; vulnery; immunomodulator;

CC antidiabetic; antisthmatic; antineumatic; antiarthritic;

CC antiinflammatory; antihyroid; antiallergic; antibacterial; antiviral;

CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;

CC neotropic; vasotropic; antipruritic and antiangiogenic. The

CC polynucleotides and polypeptides can be used for preventing, treating or

CC ameliorating medical conditions and diagnosing pathological conditions.

CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from

CC the present invention may be used to treat immune disorders by activating

CC or inhibiting the proliferation, differentiation or mobilisation of

CC immune cells, to treat disorders of haematopoietic cells, autoimmune

CC disorders, allergic reactions, graft versus host disease and organ

CC rejection, modulate haemostatic or thrombolytic activity, modulate

CC inflammation, cancers, cardiovascular disorders, neurological disease and

CC bacterial or viral infections. The peptides, nucleotides, antibodies,

CC agonists and antagonists may be also be used in drug screens. AAC78449 to

CC AAC78457 and AAB44240 represent sequences used in the exemplification of

CC the present invention

XX

SQ Sequence 61 AA;

Query Match 86.8%; Score 33; DB 3; Length 61;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
 Db 37 WMLSPFS 43

RESULT 11
 AA018834 standard; protein; 538 AA.

XX AA018834;
 XX
 XX
 XX 29-OCT-2002 (first entry)
 XX
 XX 3' cartilage superficial zone protein coding sequence encoded protein.
 XX
 XX SZP; superficial zone protein; cartilage; lubrication; human;
 XX degenerative joint condition; arthritis; osteoporosis; trauma; CACP;
 XX chondroitin sulphate substitution consensus; antiarthritic;
 XX antirheumatic; osteopathic; antigout; antiinflammatory; dermatological;
 XX immunosuppressive.
 XX Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 114 /note="encoded by ACTACT"
 FT
 XX WO200262847-A2.
 XX 15-AUG-2002.
 XX PD 31-DEC-2001; 2001MO-US050379.
 XX PR 29-DEC-2000; 2000US-0258920P.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX (RUSH-) RUSH PRESBYTERIAN ST LUKE MEDICAL CENT.
 XX
 XX Hutchins JT, Kuettner KE, Schmid TM, Schumacher BL, Su J;
 XX Dixon EP;
 XX WPI; 2002-636585/68.
 XX DR N-PDB; AAL49079.
 XX
 XX New purified superficial zone protein (SZP) polypeptides, useful for
 XX treating degenerative joint conditions, e.g. osteoarthritis, rheumatoid
 XX arthritis, gout, spondylarthritis, synovitis, tendonitis, lupus, or
 XX osteoporosis.
 XX
 XX Claim 59; Page 86-87; 89pp; English.
 XX
 XX The present invention provides the protein and coding sequences of human
 XX superficial zone protein (SZP). The protein is involved in the
 XX lubrication of joints, and the sequences can be used in the treatment of
 XX degenerative joint conditions or to delay symptoms of a degenerative
 XX joint condition, e.g. osteoarthritis, rheumatoid arthritis, gout,
 XX psoriatic arthritis, reactive arthritis, viral or post viral arthritis,
 XX spondylarthritis, juvenile arthritis, synovitis, tendonitis, systemic
 XX lupus erythematosus, CACP, osteoporosis or trauma. The present sequence
 XX is the protein encoded by the human 3' cartilage SZP cDNA
 XX
 XX Sequence 538 AA;

Query Match 86.8%; Score 33; DB 5; Length 538;
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
 Db 305 WMLSPFS 311

RESULT 12
 AAB29778 standard; protein; 902 AA.

XX AAB29778;
 XX
 XX
 XX 28-FEB-2001 (first entry)
 XX
 XX Human MSF-derived tribonectin.
 XX
 XX Human tribonectin; MSF; megakaryocyte stimulating factor;
 XX alternative splicing; joint boundary lubricant; O-linked oligosaccharide;
 XX osteoarthritis; tribosupplementation; tissue adhesion inhibitor;
 XX friction coefficient reduction; gene therapy; antiarthritic; osteopathic.
 XX
 XX Homo sapiens.
 XX
 XX WO200064930-A2.
 XX
 XX PD 02-NOV-2000.
 XX
 XX 24-APR-2000; 2000MO-US010953.
 XX
 XX 23-APR-1999; 99US-00298970.
 XX
 XX (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
 XX
 XX Jay GD;
 XX WPI; 2001-024673/03.
 XX
 XX Novel tribonectin polypeptide useful as lubricant for treating
 XX osteoarthritis, comprises O-linked lubricating moiety.
 XX
 XX Disclosure; Fig 1; 47pp; English.
 XX
 XX The invention relates to a human tribonectin which is a product of
 XX alternative splicing of the human MSF (megakaryocyte stimulating factor)
 XX gene. The tribonectin has at least one O-linked oligosaccharide
 XX lubricating moiety and has a polypeptide sequence comprising 1-76 repeats
 XX of a motif having at least 50% identity to the sequence KEDAPT
 XX (AAB29774). The invention also relates to a nucleic acid encoding a human
 XX MSF-derived tribonectin; a biocompatible composition comprising a human
 XX tribonectin for inhibiting tissue adhesion formation; and a method of
 XX diagnosing osteoarthritis or a predisposition to osteoarthritis by
 XX measuring the amount of MSF or its fragment in a biological sample of a
 XX mammal, wherein an increased amount of MSF compared to a control
 XX indicates the presence of or predisposition to developing osteoarthritis.
 XX The tribonectin and DNA encoding it are useful in the treatment of
 XX osteoarthritis, where they may be used for lubricating mammalian joints,
 XX such as articulating joints of humans, dogs or horses. The tribonectin,
 XX when formulated as a membrane, foam, gel or fibre, is useful for
 XX inhibiting adhesion between two surfaces such as the injured tissues of a
 XX mammal, where the injury is caused by a surgical incision or trauma, or
 XX an artificial device e.g., an orthopaedic implant. In particular, one of
 XX the surfaces is pericardial tissue. DNA encoding a tribonectin may be
 XX used in gene therapy. The present sequence represents a substantial
 XX portion of a human MSF-derived tribonectin
 XX
 XX Sequence 902 AA;

Query Match 86.8%; Score 33; DB 4; Length 902;
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
 Db 811 WMLSPFS 817

```

RESULT 13
AD067713
ID AD067713 standard; protein; 933 AA.
XX
AC AD067713;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human protein sequence #2379.
XX
KM osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KM gene therapy; diagnostic marker; morbid state; osteoporosis;
KM neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KM cancer.
XX
OS Homo sapiens.
XX
PN BP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
XX
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
XX
DR N-PSDB; AD067406.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 4874; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.
XX
SQ Sequence 933 AA;

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Query Match 86.8%; Score 33; DB 8; Length 933;
Best Local Similarity 85.7%; Pred. No. 9.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 WMLSPFS 7
Db 700 WMLSPFS 706

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RESULT 14
AD203664
ID AD203664 standard; protein; 981 AA.
XX
AC AD203664;
XX
DT 02-JUN-2005 (first entry)
XX
DE PRG4-Lub.1 protein.
XX
KM lubricin; antiarthritic; osteopathic; antirheumatic; cyrostatic;

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KM cardiant; respiratory-gen.; osteoarthritis; rheumatoid arthritis;
KM neoplasm; musculoskeletal disease; immune disorder; inflammation.
XX
OS Synthetic.
XX
PN WO2005016130-A2.
XX
PD 24-FEB-2005.
XX
PF 13-AUG-2004; 2004WO-US026508.
XX
PR 14-AUG-2003; 2003US-0495741P.
XX
PA (AMHP ) WYETH.
XX
PI Flannery CR, Corcoran CJ, Freeman BA, Racie LA;
XX
DR WPI; 2005-272808/28.
XX
DR N-PSDB; AD203663.
XX
PT Novel recombinant lubricin useful for treating osteoarthritis or
PT rheumatoid arthritis, or as lubricants, anti-adhesive agent or intra
PT articular supplements for synovial joints, meniscus, tendon, peritoneum,
PT pericardium or pleura.
XX
PS Claim 11; SEQ ID NO 7; 19pp; English.
XX
CC The invention relates to an isolated lubricin protein. A lubricin
CC containing composition is useful for treating a subject which involves
CC administering same to a tissue (e.g. cartilage, synovium, meniscus,
CC tendon, peritoneum, pericardium, or pleura (preferably cartilage)) of the
CC subject (e.g. mouse, rat, cat, dog, horse or human (preferably human)).
CC The above method further involves providing an anasthetic,
CC antiinflammatory drug and antibiotic to the subject, aspirating fluid
CC from the subject, washing tissue of the subject and imaging tissue of the
CC subject. The protein is useful for treating osteoarthritis or rheumatoid
CC arthritis, or as lubricants, anti-adhesive agent or intra articular
CC supplements for synovial joints, meniscus, tendon, peritoneum,
CC pericardium or pleura. An anti-lubricin antibody is useful for treating
CC cancer e.g. synoviomias. The present sequence represents the amino acid
CC sequence of the PRG4-Lub.1 protein.
XX
SQ Sequence 981 AA;

```

```

Query Match 86.8%; Score 33; DB 9; Length 981;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 WMLSPFS 7
Db 748 WMLSPFS 754

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RESULT 15
AD203668
ID AD203668 standard; protein; 1007 AA.
XX
AC AD203668;
XX
DT 02-JUN-2005 (first entry)
XX
DE PRG4-Lub.2 protein.
XX
KM lubricin; antiarthritic; osteopathic; antirheumatic; cyrostatic;
KM cardiant; respiratory-gen.; osteoarthritis; rheumatoid arthritis;
KM neoplasm; musculoskeletal disease; immune disorder; inflammation.
XX
OS Synthetic.
XX
PN WO2005016130-A2.
XX
PD 24-FEB-2005.
XX

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PS	Claim 1, 2 and 3; Fig 1; 87pp; English.
XX	The sequence given is a full length translation from the megakaryocyte
CC	stimulating factor (MSF) precursor. The sequence covered by exons II, III
CC	and IV encodes megakaryocyte stimulating factor (MSF). This sequence is
CC	modified by the addition of an N-terminal sequence encoding a secretory
CC	leader, an initiating methionine proceeding exon II and a terminating
CC	codon following exon IV. The cDNA sequence given contains sequences
CC	derived from human megakaryocyte colony stimulating factor (meg-CSF).
CC	Exon I contains the initiating methionine, and encodes a classical
CC	mammalian protein secretion signal sequence. The sequence encoding the
CC	original meg-CSF includes exons II-IV and is thought to terminate in the
CC	region between amino acid residues 134 - 147. The primary transcript of
CC	this gene may be cleaved in different ways to yield a family of mRNAs
CC	each encoding a different MSF protein. Exons V and VI are thought to be
CC	related to the activity of the factor and are also implicated in the
CC	stability, folding and processing of the molecule. These exons are also
CC	thought to play a role in the observed synergy of MSF with other
CC	cytokines. Exons V - XII are believed to be implicated in the processing
CC	or folding of the appropriate structure of the resulting factor, i.e. one
CC	or more of these exons may contain sequences which direct proteolytic
CC	cleavage, adhesion, organisation of the cellular matrix or extracellular
CC	matrix processing. Both naturally occurring and non-naturally occurring
CC	MSFs may be characterised by various combinations of alternatively
CC	spliced exons from this sequence, with the exons spliced together in
CC	differing orders to form different members of the MSF family. (Updated on
CC	25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 1404 AA;
	Query Match 86.8%; Score 33; DB 2; Length 1404;
	Best Local Similarity 85.7%; Pred. No. 1.5e+03;
	Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0,
OY	1 WMLSAFS 7
Dd	1171 WMLSPFS 1177
RESULT 24	
ID	AAB29773 standard; protein; 1404 AA.
AA	AAB29773
XX	
AC	AAA29773;
XX	
DT	28-FEB-2001 (first entry)
XX	
DE	Human megakaryocyte stimulating factor (MSF), SEQ ID NO:1.
XX	
KW	Human MSF; megakaryocyte stimulating factor; triboneurin; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; triboneurination; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic. Homo sapiens. WO200064930-A2. 02-NOV-2000. 24-APR-2000; 2000WO-US010953. 23-APR-1999; 99US-00286970. (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER. Jay GD; WPI: 2001-024673/03. N-PsDB; AAC81498.
PT	Novel triboneurin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety.

XX	Claim 3; Page 7, 47pp; English.
PS	
CC	The invention relates to a human tribonectin which is a product of
CC	alternative splicing of the human MSF (megakaryocyte stimulating factor)
CC	gene. The tribonectin has at least one O-linked oligosaccharide
CC	lubricating moiety and has a polypeptide sequence comprising 1-76 repeats
CC	of a motif having at least 50% identity to the sequence KEPAPT
CC	(AAB29774). The invention also relates to a nucleic acid encoding a human
CC	MSF-derived tribonectin; a biocompatible composition comprising a human
CC	tribonectin for inhibiting tissue adhesion formation; and a method of
CC	diagnosing osteoarthritis or a predisposition to osteoarthritis by
CC	measuring the amount of MSF or its fragment in a biological sample of a
CC	mammal, wherein an increased amount of MSF compared to a control
CC	indicates the presence of or predisposition to developing osteoarthritis.
CC	The tribonectin and DNA encoding it are useful in the treatment of
CC	osteoarthritis, where they may be used for lubricating mammalian joints,
CC	such as articulating joints of humans, dogs or horses. The tribonectin,
CC	when formulated as a membrane, foam, gel or fibre, is useful for
CC	inhibiting adhesion between two surfaces such as the injured tissues of a
CC	mammal, where the injury is caused by a surgical insertion or trauma, or
CC	an artificial device e.g., an orthopaedic implant. In particular, one of
CC	the surfaces is pericardial tissue. DNA encoding a tribonectin may be
CC	used in gene therapy. The present sequence represents human MSF
CC	
SO	Sequence 1404 AA;
Qy	Query Match 86.8%; Score 33; DB 4; Length 1404;
Db	Best local similarity 85.7%; Pred. No. 1.5e+03;
	Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	1 WMLSAFS 7
	1171 WMLSPFS 1177
RESULT 25	
AAB60568	
ID	AAB60568 standard; protein; 1404 AA.
AC	AAB60568;
DT	27-APR-2001 (first entry)
DE	Human megakaryocyte stimulating factor (MSF, CACP).
KW	Human; CACP protein; campodactylly-arthropathy-coxa vara-pericarditis;
KW	MSF; megakaryocyte stimulating factor; synovial lubricant;
KW	chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
KW	antiarthritic.
OS	Homo sapiens.
PN	WO200107068-A1.
PD	01-FEB-2001.
PF	21-JUL-2000; 2000WO-US020002.
PR	23-JUL-1999; 99US-0145328P.
PR	19-JUL-2000; 2000US-00145328.
PA	(UYCA-) UNIV CASE WESTERN RESERVE.
PI	Warman ML;
DR	WPI; 2001-182721/18.
PT	New composition comprising the campodactylly-arthropathy-coxa vara-
PT	pericarditis protein in combination with an anesthetic, useful for
PT	treating osteoarthritis, or as lubricants of tissue and joints.
PS	Example 1; Page; 34pp; English.

OY 1 WMLSAFS 7
 |||||
 DB 1171 WMLSPFS 1177

RESULT 28
 ADX69335

ID ADX69335 standard; protein; 1404 AA.

AC ADX69335;

DT 05-MAY-2005 (first entry)

DE Human heparin binding protein #35.

XX Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian;
 XX Anticonvulsant; VEGF-3 receptor; Angiogenesis stimulator; Gene Therapy;
 KW Vascular endothelial growth factor receptor 3; VEGFR-3;
 KW angiogenesis disorder; neurodegenerative disorder; Alzheimers disease;
 KW Parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C;
 KW neurological disease; Huntingtons chorea;
 KW vascular endothelial growth factor receptor 3; neurological disease.

OS Homo sapiens.

PN WO2005016963-A2.

PD 24-FEB-2005.

PF 14-JUN-2004; 2004WO-US019122.

PR 12-JUN-2003; 2003US-0478114P.

PR 12-JUN-2003; 2003US-0478390P.

PR 23-SEP-2003; 2003US-00669176.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA LTD.

PI Alitalo K, He Y, Tammela T;

DR WPI; 2005-182331/19.

XX New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands

PT comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for

PT treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or

PT Huntington's disease.

PS Disclosure; SEQ ID NO 55; 219pp; English.

XX The invention relates to heparin-binding vascular endothelial growth

CC factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The

CC heparin binding VEGFR-3 proteins are used for stimulating

CC lymphangiogenesis or angiogenesis in a mammal, and for modulating the

CC growth of mammalian endothelial cells, mammalian endothelial precursor

CC cells or hematopoietic progenitor cells. The polypeptide may also be used

CC for promoting recruitment, proliferation, differentiation, migration or

CC survival of neuronal cells or neuronal precursor cells, and for treating

CC neurodegenerative disorder, e.g. Alzheimer's disease, Parkinson's

CC disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral

CC Sclerosis (ALS), dementia, or cerebral palsy. The present sequence

CC represents a human heparin binding protein of the invention.

XX Sequence 1404 AA;

Query Match 86.8%; Score 33; DB 9; Length 1404;

Best Local Similarity 85.7%; Pred. No. 1.5e+03;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 DB 1171 WMLSPFS 1177

RESULT 29
 ADY15658
 ID ADY15658 standard; protein; 1404 AA.

AC ADY15658;

DT 05-MAY-2005 (first entry)

DE PRO polypeptide SEQ ID NO 1464.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 KW Vinorelbine; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; ds; gene; diagnosis.

OS Homo sapiens.

PN WO2005016962-A2.

PD 24-FEB-2005.

PF 11-AUG-2004; 2004WO-US026249.

PR 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

DR WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and

PT treating an immune related disorder, e.g. systemic lupus erythematosus,

PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 1464; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a DNA encoding a PRO
 CC polypeptide.

XX Sequence 1404 AA;

Query Match 86.8%; Score 33; DB 9; Length 1404;

Best Local Similarity 85.7%; Pred. No. 1.5e+03;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 DB 1171 WMLSPFS 1177

RESULT 30

ADX66477
 ID AED66477 standard; protein; 1404 AA.

AC AED66477;

DT 29-DEC-2005 (first entry)

DE Human lubricin protein sequence.

XX Wound healing agent; tissue regeneration; antisense therapy; trauma;
 KW vulnery; injury; fractures; osteopathic; synovitis; inflammation;
 KW lubricin.

OS Homo sapiens.

PN WO2005102363-A2.

[illegible]

XX	PI	Jay G;
XX	DR	WPI; 2006-136979/14.
XX	DR	N-PSDB; AEF54257.
XX	PT	Visco-supplementation composition, useful for the lubrication and
XX	PT	chondroprotection of mammalian joint, comprising hyaluronic acid and
XX	PT	tribonectin.
XX	PS	Disclosure; SEQ ID NO 1; 50pp; English.
XX	CC	The invention relates to a viscosupplementation composition (A) which
XX	CC	comprises hyaluronic acid (1-5 mg/ml) and tribonectin (10-250 mu g/ml).
XX	CC	Also described is the use of tribonectin in the preparation of a
XX	CC	medicament for the lubrication and chondroprotection of a mammalian
XX	CC	joint, where the tribonectin is added to a visco-supplement in the
XX	CC	preparation of the medicament, which increases the elasticity of the
XX	CC	visco-supplement. (A) is useful in the preparation of medicament for the
XX	CC	lubrication or chondroprotection of a mammalian joint (particularly
XX	CC	articulating a joint of a human, horse or dog). The present sequence
XX	CC	represents human megakaryocyte stimulating factor (MSF).
XX	SEQ	Sequence 1404 AA;
XX	Query Match	86.8%; Score 33; DB 10; Length 1404;
XX	Best Local Similarity	85.7%; Pred. No. 1.5e+03;
XX	Matches	6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	OY	1 WMLSAFS 7
XX		
XX	Db	1171 WMLSPFS 1177
XX	RESULT 32	
XX	ID	AEF89839
XX	ID	AEF89839 standard; protein; 1404 AA.
XX	AC	AEF89839;
XX	DT	20-APR-2006 (first entry)
XX	DE	Human megakaryocyte stimulating factor (MSF) - SEQ ID 1.
XX	KX	tribonectin; arthritis; antiarthritic; osteoarthritis; osteopathic;
XX	KW	megakaryocyte stimulating factor; MSF.
XX	OS	Homo sapiens.
XX	PN	US7001861-B1.
XX	PD	21-FEB-2006.
XX	PF	24-APR-2000; 2000US-00556246.
XX	PR	23-APR-1999; 99US-00298970.
XX	PA	(RHOD-) RHODE ISLAND HOSPITAL.
XX	PI	Jay GD;
XX	DR	WPI; 2006-170699/18.
XX	DR	N-PSDB; AEF89840.
XX	PT	New isolated tribonectin comprising a boundary-lubricating amount of
XX	PT	polypeptide, and an O-linked oligosaccharide group, for use in treating
XX	PT	arthritic diseases, and to coat artificial limbs and joints.
XX	PS	Claim 1; SEQ ID NO 1; 34pp; English.
XX	CC	The invention comprises a tribonectin protein (a boundary lubricating
XX	CC	polypeptide), the tribonectin protein of the invention comprises the
XX	CC	human megakaryocyte stimulating factor (MSF) protein. The tribonectin

CC protein of the invention is useful for treating arthritic disease and
CC osteoarthritis disease, and for coating artificial limbs and joints prior
CC to implantation. The present amino acid sequence represents the human MSF
CC protein of the invention.
XX

SQ Sequence 1404 AA;

Query Match 86.8%; Score 33; DB 10; Length 1404;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|||
|||

Db 1171 WMLSPFS 1177

RESULT 33
AAU32262

ID AAU32262 standard; protein; 1415 AA.

XX AAU32262;

XX 18-DEC-2001 (first entry)

DE Novel human secreted protein #2753.

XX Human; vaccination; gene therapy; nutritional supplement;
KM stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US008656.

XX 18-APR-2000; 2000US-00552929.

PR 26-JAN-2001; 2001US-00770160.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-611725/70.

DR Nucleic acids encoding a range of human polypeptides, useful in genetic

XX vaccination, testing and therapy.

XX Claim 20; Page 573; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represents the amino acid sequences of novel human
CC secreted proteins of the invention

XX Sequence 1415 AA;

Query Match 86.8%; Score 33; DB 4; Length 1415;

Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|||
|||

Db 1182 WMLSPFS 1188

RESULT 34

AAU82730

ID AAU82730 standard; protein; 31 AA.

XX AAU82730;

XX 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen SEQ ID NO:10323.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis.

XX Homo sapiens.

PN WO200157182-A2.

PD 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226682P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235835P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 DR N-PSDB; AAK5511.
 DR
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Claim 11; SEQ ID NO 10323; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54950 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 CC
 XX
 SQ Sequence 31 AA;
 Query Match 84.2%; Score 32; DB 4; Length 31;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WMLSAFS 7
 Db 6 WMLSAFS 12
 RESULT 35
 ABP04103
 ID ABP04103 standard; protein; 81 AA.
 XX
 AC ABP04103;
 XX
 DT 25-JUN-2002 (first entry)
 XX
 DE Human ORFX protein sequence SEQ ID NO:8188.
 XX
 KW Human, open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypotension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 XX Homo sapiens.
 OS
 PN WO200192523-A2.
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001MO-US010836.
 XX
 PR 30-MAY-2000; 2000US-0206132P.
 PR 29-AUG-2000; 2000US-0228716P.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach MD;
 XX
 DR WPI; 2002-106308/14.
 DR N-PsDB; ABN19855.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX
 PS Disclosure; SEQ ID NO 8188; 1037bp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 81 AA;
 QY
 Query Match 84.2%; Score 32; DB 5; Length 81;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 1 WMLSAFS 7
 68 WLSAYS 74
 RESULT 36
 ADC95262
 ID ADC95262 standard; protein; 103 AA.
 XX
 AC ADC95262;
 XX

DT 01-JAN-2004 (first entry)
 XX
 DE E. faecium protein sequence SEQ ID 4889.
 XX
 KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.
 XX
 OS Enterococcus faecium.
 XX
 PN US6583275-B1.
 PD 24-JUN-2003.
 XX
 PF 30-JUN-1998; 98US-00107532.
 XX
 PR 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Doucette-Stamm LA, Bush D;
 XX
 DR WPI; 2003-799836/75.
 DR N-PsDB; ADC91608.
 XX
 PT New isolated nucleic acid derived from Enterococcus faecium encoding an
 PT Enterococcus faecium polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 XX
 PS Example 1; SEQ ID NO 4889; 243bp; English.
 XX
 CC The invention relates to an isolated nucleic acid derived from
 CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridizing to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from E. faecium bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of Candida albicans -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating Enterococcus faecium infections. The present sequence represents
 CC one if the disclosed E. faecium proteins.
 XX
 SQ Sequence 103 AA;
 QY
 Query Match 84.2%; Score 32; DB 7; Length 103;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 WMLSAF 6
 17 WMLSAF 22
 RESULT 37
 AAU25590
 ID AAU25590 standard; protein; 211 AA.
 XX
 AC AAU25590;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human G Protein-Coupled Receptor (GPCR) polypeptide #37.
 XX
 KW Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;

XX	attentional deficit disorder; anxiety; depression; bipolar disorder;
KM	neurological disorder; Huntington's disease; dementia; obesity; anorexia;
KM	metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
KM	type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
KM	cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
KM	viral infection; immunostimulant; neuroleptic; nootropic; tranquilizer;
XX	antidepressant; anorectic; gene therapy.
OS	
XX	Homo sapiens.
XX	
PN	WO200162797-A2.
PD	
XX	30-AUG-2001.
XX	
PE	23-FEB-2001; 2001WO-US005676.
XX	
PR	23-FEB-2000; 2000US-0184247P.
PR	23-FEB-2000; 2000US-0184303P.
PR	23-FEB-2000; 2000US-0184304P.
PR	23-FEB-2000; 2000US-0184305P.
PR	23-FEB-2000; 2000US-0184397P.
PR	02-MAR-2000; 2000US-0186457P.
PR	03-MAR-2000; 2000US-0186810P.
PR	09-MAR-2000; 2000US-0188064P.
PR	13-MAR-2000; 2000US-0188880P.
PR	03-APR-2000; 2000US-0194344P.
PR	23-JUN-2000; 2000US-0213861P.
PR	11-JUL-2000; 2000US-0217369P.
PR	11-JUL-2000; 2000US-0217370P.
PR	14-JUL-2000; 2000US-0218337P.
PR	20-JUL-2000; 2000US-0218492P.
XX	
PA	(PHAA) PHARMACIA & UPJOHN CO.
XX	
PI	Vogel I G, Wood LS, Parodi LA, Lind P;
XX	
DR	WPI; 2001-570628/64.
DR	N-PSDB; AAS42842.
XX	
PT	New isolated nucleic acid encoding a new G-protein coupled receptor
PT	polypeptide for detecting receptor modulators that can treat mental
XX	disorders, such as schizophrenia, anxiety, depression, or obesity.
XX	
PS	Claim 35; Page 84; 279pp; English.
CC	
CC	Sequences AAU25554-AAU55616 represent human G-protein coupled receptor
CC	(GPCR) polypeptides of the invention. The proteins and their associated
CC	DNA sequences can be used to identify compounds which bind to GPCR
CC	polypeptides and in screening for compounds that modulate GPCR activity,
CC	By screening a human subject for the presence of mutations in GPCR DNA, a
CC	GPCR-related disorder or a genetic predisposition can be diagnosed. The
CC	sequences can also be used for treatment and prevention of mental
CC	disorders such as schizophrenia, attention deficit disorder, anxiety,
CC	depression, dementia and bipolar disorder, neurological disorders such as
CC	Huntington's disease, Parkinson's disease and Tourette's syndrome,
CC	metabolic disorders such as obesity, anorexia and type 2 diabetes,
CC	cardiovascular disorders such as thrombosis, myocardial infarction,
CC	cardiomyopathy and atherosclerosis, viral infections caused by HIV and
CC	cancers
XX	
XX	Sequence 211 AA;
SO	
Query Match	84.2%; Score 32; DB 4; Length 211;
Best Local Similarity	71.4%; Pred. No. 3.1e+02;
Matches	5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 WMLSAFS 7	
128 WMLAIFS 134	

RESULT 38
ADR09699

ID	ADR09699	standard; protein; 243 AA.
AC	ADR09699;	
DT	04-NOV-2004	(first entry)
DE	Human protein useful for treating neurological disease seq 3205.	
XX	human; oligo-capping method; diagnostic marker; gene therapy;	
KM	osteoporosis; neurological disease; Alzheimer's disease;	
KM	Parkinson's disease; dementia; short memory; cancer;	
KM	sense or motor function; emotional reaction; fear response; panic;	
KM	osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;	
XX	tranquilliser.	
OS	Homo sapiens.	
PN	EP1447413-A2.	
XX	18-AUG-2004.	
PD	12-FEB-2004; 2004EP-00003145.	
PF	14-FEB-2003; 2003JP-00102207.	
XX	09-MAY-2003; 2003JP-00131452.	
PR	(REAS-) RES ASSOC BIOTECHNOLOGY.	
PA	Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;	
P1	Wakamatsu A, Ishii S, Nagai K, Irie R;	
XX	WPI; 2004-583265/57.	
DR	N-PSDB; ADR07743.	
XX	New 1995 cDNA, useful for treating osteoporosis, neurological diseases,	
PT	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.	
PS	Claim 1; SEQ ID NO 3205; 2686pp; English.	
XX	This invention relates to novel, isolated full length human cDNA	
CC	molecules and the encoded proteins thereof. Specifically, it refers to	
CC	cDNA clones obtained by an oligo-capping method, where none of these	
CC	clones are identical to any known human mRNAs. The present invention	
CC	describes an immunoassay to identify agonists and antagonists, as well as	
CC	antibodies, antisense molecules and siRNAs that can all be used to bind	
CC	to and modulate expression of the cDNA molecules. As such, these	
CC	molecules are useful for diagnostic markers or therapeutic targets for	
CC	the various diseases or morbid states. In particular, they are useful in	
CC	gene therapy for treating osteoporosis, neurological disease, Alzheimer's	
CC	disease, Parkinson's disease, dementia, short memory and various cancers,	
CC	as well as for maintaining equilibrium of sense or motor function, and	
CC	for treating emotional reaction, fear response and panic. Accordingly,	
CC	they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,	
CC	cyostatic and tranquilliser activities. This polypeptide is a protein	
CC	encoded by a full length human cDNA sequence of the invention. NOTE: This	
CC	sequence is not given in the sequence listing of the specification but	
CC	can be obtained on CD-ROM from the European Patent Office, Vienna Sub-	
CC	office.	
XX	Sequence 243 AA;	
QY	Query Match	84.2%; Score 32; DB 8; Length 243;
DB	Best Local Similarity	85.7%; Pred. No. 3.6e+02;
	Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
	1 WMLSAFS 7	
	187 WMLSAFS 193	

RESULT	39
ABO	73613
ID	ABO7

XX AB073613;
AC 29-JUL-2004. (first entry)
XX
XX
XX Pseudomonas aeruginosa polypeptide #5788.
DE
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX Pseudomonas aeruginosa.
OS
XX US6551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI WPI; 2003-615309/58.
XX
XX N-PSDB; ABD07184.
DR
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 22359; 455bp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnosis,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences AB067826-
XX AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 262 AA;
SQ
Query Match 84.2%; Score 32; DB 7; Length 262;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
Db 234 WMLSAIS 240
RESULT 40
AAG81234
ID AAG81234 standard; protein; 280 AA.
XX
XX AAG81234;
AC
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target protein SEQ ID 283.
DE
XX Drug target; growth; organism viability; characterisation.
XX

OS Mycobacterium tuberculosis.
XX
XX WO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-US031152.
XX
XX 12-NOV-1999; 99US-0165086P.
XX 12-NOV-1999; 99US-0165124P.
XX 01-FEB-2000; 2000US-0179531P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
PI WPI; 2001-329193/34.
XX
XX N-PSDB; AAH52085.
DR
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the sequences.
XX
XX Disclosure; Page 190; 207pp; English.
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The
XX method involves providing an unknown nucleotide or polypeptide sequences,
XX and comparing it to a number of sequences along with at least one
XX algorithm capable of analysing a functional relationship between
XX nucleotide and polypeptide sequences. The method is useful for
XX characterising the function of nucleic acids and polypeptides that may be
XX useful as a target for a drug or essential for the growth or viability of
XX an organism
XX
XX Sequence 280 AA;
SQ
Query Match 84.2%; Score 32; DB 4; Length 280;
Best Local Similarity 71.4%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
Db 262 WMLAAFA 268
RESULT 41
AAM51647
ID AAM51647 standard; protein; 289 AA.
XX
XX AAM51647;
AC
XX
XX 20-FEB-2002 (first entry)
XX
XX Human GPCR polypeptide.
DE
XX Human, G-protein coupled receptor; GPCR; gene therapy;
XX MAS proto-oncogene receptor; human protease; disease.
XX Homo sapiens.
XX
XX WO200181409-A2.
XX
XX 01-NOV-2001.
XX
XX 24-APR-2001; 2001WO-US013097.
XX
XX 24-APR-2000; 2000US-0199149P.
XX 04-AUG-2000; 2000US-00633146.
XX

XX (PEKE) PE CORP NY.
 XX
 PI Wei M, Cravchik A, Di Francesco V, Beasley EM;
 XX
 DR WPI: 2002-0469265/06.
 DR N-PSDB; ABA03701.
 XX
 PT Novel human G protein-coupled receptor polypeptide that is related to MAS
 PT proto-oncogene receptor subfamily, useful as model and target for
 PT developing human therapeutic agent.
 XX
 PS Claim 1; Fig 2; 60pp; English.
 XX
 CC The invention relates to an isolated human G protein-coupled receptor
 CC (GPCR) polypeptide that is related to the MAS proto-oncogene receptor
 CC subfamily. The polypeptide comprises a fully defined sequence of 289
 CC amino acids as given in the specification, or its fragment comprising 10
 CC contiguous amino acids, or an amino acid sequence of an allelic variant
 CC or orthologue of the amino acid sequence given in the sequence. The
 CC polypeptide is useful for identifying a modulator of a GPCR polypeptide
 CC or an agent that binds to it. The polypeptide is also useful for
 CC treating a disease or condition mediated by human proteases. The present
 CC sequence is the polypeptide of the invention
 XX
 SQ Sequence 289 AA;
 Query Match 84.2%; Score 32; DB 5; Length 289;
 Best Local Similarity 71.4%; Pred. No. 4.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 WMLSAFS 7
 Db 94 WMLAAPS 100
 XX
 RESULT 42
 ADO29555 standard; protein; 289 AA.
 XX
 AC ADO29555;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Mouse GPCR N8 (MRGG), SEQ ID NO:657.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
 KW cytoskeletal; antiinflammatory; vasotropic; antitaxonal; antitachycardic;
 KW CNS; central nervous system; respiratory; antidiabetic; antihypertensive;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 KW murine; receptor.
 XX
 OS Mus musculus.
 XX
 PN WO2004040000-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-USO28226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461322P.
 XX

PA (PRIM-) PRIMAL INC.
 XX
 PI Galtanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vaessiliatis D, Zeng H;
 XX
 DR WPI: 2004-390329/36.
 DR N-PSDB; ADO30286.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 657, 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCR) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice, kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 289 AA;
 Query Match 84.2%; Score 32; DB 8; Length 289;
 Best Local Similarity 71.4%; Pred. No. 4.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 WMLSAFS 7
 Db 94 WMLAAPS 100
 XX
 RESULT 43
 ADO29554 standard; protein; 289 AA.
 XX
 AC ADO29554;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human GPCR N8 (MRGG), SEQ ID NO:656.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW

KM kidney disorder; liver disorder; lung disorder; breast disorder;
 KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KM thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KM cytoskeletal; antiinflammatory; vasotropic; antidiarrhoeal; antidiabetic;
 KM CNS; central nervous system; respiratory; antidiarrhoeal; antidiabetic;
 KM virolytic; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KM dermatological; antitumor; anticholesteric; antiallergic; anorectic;
 KM immunosuppressive; nephroretropic; gene therapy; GPCR modulator; human;
 KM receptor.
 KM Homo sapiens.
 OS
 XX
 XX WO2004040000-A2.
 PN
 PD 13-MAY-2004.
 PF
 XX 09-SEP-2003; 2003MO-US028226.
 PF
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 PR
 XX (PRIM-) PRIMAL INC.
 PA
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX
 XX WPI; 2004-390329/36.
 DR N-PDB; ADO29996.
 DR
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 PT
 XX
 XX Claim 151; SEQ ID NO 656; 542pp; English.
 PS
 XX
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 289 AA;

Query March 84.2%; Score 32; DB 8; Length 289;
 Best Local Similarity 71.4%; Pred. No. 4.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMLSARS 7
 Db 94 WMLAAPS 100
 RESULT 44
 AAU25612
 ID AAU25612 standard; protein; 323 AA.
 XX
 AC AAU25612;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human G Protein-Coupled Receptor (GPCR) polypeptide #59.
 XX
 XX Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
 KM attention deficit disorder; anxiety; depression; bipolar disorder;
 KM neurological disorder; Huntington's disease; dementia; obesity; anorexia;
 KM metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
 KM type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
 KM cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
 KM viral infection; immunostimulant; neuroleptic; nootropic; tranquilliser;
 KM antidepressant; anorectic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200162797-A2.
 PD 30-AUG-2001.
 PF
 XX 23-FEB-2001; 2001MO-US005676.
 XX
 XX 23-FEB-2000; 2000US-0184247P.
 PR 23-FEB-2000; 2000US-0184303P.
 PR 23-FEB-2000; 2000US-0184304P.
 PR 23-FEB-2000; 2000US-0184305P.
 PR 23-FEB-2000; 2000US-0184397P.
 PR 02-MAR-2000; 2000US-0186457P.
 PR 03-MAR-2000; 2000US-0186810P.
 PR 09-MAR-2000; 2000US-0188064P.
 PR 13-MAR-2000; 2000US-0188880P.
 PR 03-APR-2000; 2000US-0194344P.
 PR 23-JUN-2000; 2000US-0213861P.
 PR 11-JUL-2000; 2000US-0217369P.
 PR 11-JUL-2000; 2000US-0217370P.
 PR 14-JUL-2000; 2000US-0218337P.
 PR 20-JUL-2000; 2000US-0218492P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Vogel I G, Wood LS, Parodi LA, Lind P;
 PI
 XX WPI; 2001-570628/64.
 DR N-PDB; AAS42864.
 DR
 XX
 PT New isolated nucleic acid encoding a new G-protein coupled receptor
 PT polypeptide for detecting receptor modulators that can treat mental
 PT disorders, such as schizophrenia, anxiety, depression, or obesity.
 XX
 PS Claim 35; Page 94; 279pp; English.
 XX
 XX Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
 CC (GPCR) polypeptides of the invention. The proteins and their associated
 CC DNA sequences can be used to identify compounds which bind to GPCR
 CC polypeptides and in screening for compounds that modulate GPCR activity.
 CC By screening a human subject for the presence of mutations in GPCR DNA, a
 CC GPCR-related disorder or a genetic predisposition can be diagnosed. The
 CC sequences can also be used for treatment and prevention of mental
 CC disorders such as schizophrenia, attention deficit disorder, anxiety,
 CC depression, dementia and bipolar disorder, neurological disorders such as
 CC Huntington's disease, Parkinson's disease and Tourette's syndrome.

CC metabolic disorders such as obesity, anorexia and type 2 diabetes,
 CC cardiovascular disorders such as thrombosis, myocardial infarction,
 CC cardiomyopathy and atherosclerosis, viral infections caused by HIV and
 CC cancers

XX
 SQ Sequence 323 AA;

Query Match 84.2%; Score 32; DB 4; Length 323;
 Best Local Similarity 71.4%; Pred. No. 4.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
 Db 128 WMLAIFS 134

RESULT 45
 ABB06257
 ID ABB06257 standard; protein; 323 AA.

XX ABB06257;

XX 23-MAY-2002 (first entry)

DE Human G protein-coupled receptor TGR15 protein SEQ ID NO:1.

XX Human; G protein-coupled receptor; TGR15; nocotropic; antiinflammatory;
 KM vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;
 KM neurological; inflammatory; circulatory; degenerative; immune system;
 KM digestive disease; cancer.

XX Homo sapiens.

XX W0200204639-A1.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-JP005876.

XX 07-JUL-2000; 2000JP-00211987.

XX 26-DEC-2000; 2000JP-00395566.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Moriya T, Ito T, Shintani Y, Miyajima N;

XX WPI: 2002-179705/23.

XX N-PSDB; ABL40211.

PT G-protein coupled receptor protein TGR15 of human origin and DNA encoding
 PT it for diagnosis and treatment of cancer and circulatory and other
 PT diseases associated with its expression.

XX Claim 1; Fig 2; 103pp; Japanese.

XX The present sequence represents a human guanine nucleotide binding
 CC protein (G protein)-coupled receptor protein designated TGR15. TGR15 has
 CC nocotropic, antiinflammatory, vasotropic, immunomodulator and cytostatic
 CC activities. The TGR15 polynucleotide and protein can be used in gene
 CC therapy and protein therapy. G-protein coupled receptor proteins are cell
 CC membrane proteins which mediate the cellular response to a large variety
 CC of signalling molecules. The TGR15 polynucleotide and protein can be used
 CC in the diagnosis, treatment and prevention of diseases including
 CC neurological, inflammatory, circulatory, degenerative, immune system and
 CC digestive diseases and cancer

XX Sequence 323 AA;

Query Match 84.2%; Score 32; DB 5; Length 323;
 Best Local Similarity 71.4%; Pred. No. 4.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7

Db 128 WMLAIFS 134

RESULT 46
 ABB10905
 ID ABB10905 standard; protein; 371 AA.

XX ABB10905;

DT 05-DEC-2002 (first entry)

DE Human secreted protein (SECP) #1.

XX Human; gene therapy; secreted protein; SECP; hepatitis; cancer;
 KM cell proliferative disorder; autoimmune disorder; inflammatory disorder;
 KM AIDS; asthma; anaemia; allergy; atopic dermatitis; myocardial infarction;
 KM cardiovascular disorder; vascular tumour; neurological disorder; stroke;
 KM epilepsy; cerebral neoplasm; Alzheimer's disease; developmental disorder;
 KM Cushing's syndrome; muscular dystrophy.

XX Homo sapiens.

XX W0200270669-A2.

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US007719.

XX 06-MAR-2001; 2001US-0273946P.

XX 16-MAR-2001; 2001US-0276873P.

XX 30-MAR-2001; 2001US-0280531P.

XX 30-MAR-2001; 2001US-0280596P.

XX 16-NOV-2001; 2001US-0332426P.

XX 28-NOV-2001; 2001US-0334229P.

XX 11-JAN-2002; 2002US-0347703P.

XX WPI: 2002-713444/77.

XX N-PSDB; ABL11179.

PT New human secreted proteins and nucleic acids useful in diagnosing,
 PT treating and preventing cell proliferative, autoimmune/inflammatory,
 PT cardiovascular, neurological, and developmental disorders.

XX Claim 1; Page 126-127; 162pp; English.

XX The invention comprises the amino acid and coding sequences of human
 CC secreted proteins (SECP). The human SECP DNA and protein sequences of the
 CC invention are useful for the treatment and prevention of cell
 CC proliferative disorders (e.g. actinic keratosis, arteriosclerosis,
 CC bursitis, hepatitis or cancer); autoimmune/inflammatory disorders (e.g.
 CC AIDS, asthma, anaemia, allergies or atopic dermatitis); cardiovascular
 CC disorders (e.g. congestive heart failure, ischaemic heart disease,
 CC myocardial infarction, hypertensive heart disease, or vascular tumours);
 CC neurological disorders (e.g. epilepsy, stroke, cerebral neoplasms, or
 CC Alzheimer's disease); and developmental disorders (e.g. renal tubular
 CC acidosis, Cushing's syndrome, Duchenne and Becker muscular dystrophy, or
 CC hypothyroidism). The present amino acid sequence represents a human
 CC secreted protein (SECP) of the invention

XX Sequence 371 AA;

Query Match 84.2%; Score 32; DB 5; Length 371;
 Best Local Similarity 85.7%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 DB 187 WMLSAFS 193

RESULT 47

ID ABO60886 standard; protein; 437 AA.

AC ABO60886;

DT 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 7403.

XX Recombinant expression vector; transcription regulatory element;

XX Klebsiella pneumoniae protein; antibacterial; Vaccine.

OS Klebsiella pneumoniae.

PN US610836-B1.

PD 26-AUG-2003.

PF 27-JAN-2000; 2000US-00489039.

PR 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PI Breton GL, Osborne M;

XX WPI; 2003-895346/82.

DR N-PSDB; ACH94437.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for

PT preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 7403; 932pp; English.

CC The invention describes a new isolated nucleic acid encoding a Klebsiella

CC pneumoniae polypeptide. Also described are: a recombinant expression

CC vector comprising the nucleic acid, operably linked to a transcription

CC regulatory element; and a cell comprising the recombinant expression

CC vector. The nucleic acid is useful for preparing a vaccine composition

CC against Klebsiella pneumoniae. This is the amino acid sequence of a

CC Klebsiella pneumoniae polypeptide of the invention

XX Sequence 437 AA;

OY 1 WMLSAFS 7

DB 391 WMLSAFS 397

RESULT 48

ID ADF70484 standard; protein; 561 AA.

AC ADF70484;

DT 12-FEB-2004 (first entry)

XX Orphan receptor ligand-related human protein SeqID107.

XX ligand; orphan receptor protein; fusion protein; fluorescent protein;

XX cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;

XX GFPuv; Enhanced GFP; EGFP; human.

OS Homo sapiens.

PN WO2003071272-A1.

PD 28-AUG-2003.

PF 21-FEB-2003; 2003WO-JP001901.

PR 22-FEB-2002; 2002JP-00045728.

PR 23-JUL-2002; 2002JP-0021949.

PR 11-OCT-2002; 2002JP-00298237.

XX (TAKE) TAKEDA CHEM IND LTD.

PA Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;

XX WPI; 2003-697654/66.

DR N-PSDB; ADF70586.

XX Transformation of cells with a fusion protein of an orphan receptor

PT protein with a fluorescent protein useful for identification of ligands

XX to the orphan receptor.

XX Disclosure; SEQ ID NO 107; 594pp; Japanese.

XX This invention relates to a novel method of identifying ligands to an

XX orphan receptor protein which comprises transforming cells with DNA

XX encoding a fusion protein of the orphan receptor with a fluorescent

XX protein, so that the fusion protein is expressed in the cells (or cell

XX membranes isolated from them) and contacting the cells with the potential

XX ligand to be tested. A suitable fluorescent protein for incorporation in

XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,

XX wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the

XX identification of ligands binding to an orphan receptor protein.

XX Sequence 561 AA;

OY 1 WMLSAFS 7

DB 128 WMLSAFS 134

RESULT 49

ID ADU02401 standard; protein; 1180 AA.

AC ADU02401;

DT 27-JAN-2005 (first entry)

XX Novel human polypeptide seqid 868.

XX cytosolic; antiapoptotic; antiinflammatory; gene therapy; Nanodisc;

XX proliferative disorder; inflammatory disorder; immune disorder;

XX metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;

XX ulcerative colitis; human.

XX Homo sapiens.

XX WO2004093804-A2.

XX 04-NOV-2004.

XX 19-APR-2004; 2004WO-US012047.

XX 18-APR-2003; 2003US-0463708P.

XX 18-APR-2003; 2003US-0463732P.

XX 02-MAY-2003; 2003US-0467199P.

XX 02-MAY-2003; 2003US-0467230P.

PR 19-MAY-2003; 2003US-0471306P.
 PR 19-MAY-2003; 2003US-0471336P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.
 PR 08-SEP-2003; 2003US-0505059P.
 XX
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 XX
 PI Lee E, Hestir K, Chu K, Masuoka L, Williams LT;
 XX
 DR WPI; 2004-775861/76.
 DR N-PSDB; ADU01669.
 XX
 PT New first nucleic acid molecule comprising a polynucleotide sequence
 PT diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
 XX
 PS Claim 14; SEQ ID NO 868; 291bp; English.

CC The invention describes a new first nucleic acid molecule comprising a
 CC polynucleotide sequence given in the specification. Also described are:
 CC an animal injected with the nucleic acid molecule; a second nucleic acid
 CC molecule comprising a second polynucleotide sequence that is at least
 CC about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or
 CC that hybridizes to the first polynucleotide sequence under high
 CC stringency conditions; a vector comprising the nucleic acid molecule and
 CC a promoter that drives the expression of the nucleic acid molecule; a
 CC host cell transformed, transfected, transduced or infected with the
 CC nucleic acid molecule; a nucleic acid composition comprising a carrier or
 CC a buffer and one or more compositions comprising the nucleic acid
 CC molecule, vector or host cell; a substantially purified polypeptide; an
 CC animal injected with the polypeptide; a polypeptide composition
 CC comprising the polypeptide molecule and a carrier or buffer; a cell
 CC culture medium comprising the polypeptide or transfected cells
 CC transfected with the polynucleotide; making a transformed, transfected,
 CC transduced, or infected host cell; synthesizing Nanodiscs simultaneously
 CC and for synthesising a series of simultaneously-synthesised Nanodiscs
 CC sequentially utilising a dynamic system; preparing a hydrophobic protein
 CC for determination of crystal structure; immunising a non-human animal;
 CC screening for modulators of hydrophobic protein activity; a diagnostic
 CC kit; determining the presence of the nucleic acid molecule or its
 CC complement; determining the presence of an antibody to the polypeptide in
 CC a sample; an antibody specifically recognising, binding to or modulating
 CC the biological activity of at least one polypeptide encoded by a nucleic
 CC acid molecule or its biologically active fragment; an antibody
 CC composition comprising the antibody and a carrier; a bacteriophage, where
 CC the antibody is displayed on the bacteriophage; a bacterial cell
 CC comprising the bacteriophage; a non-human animal injected with the
 CC antibody composition; a host cell that secretes the antibody; making an
 CC antibody; diagnosing a disease, disorder, syndrome, or condition
 CC comprising cancer, or proliferative, inflammatory, immune, metabolic,
 CC bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
 CC conditions in a patient; a modulator composition comprising a modulator
 CC and a carrier; gene therapy; prophylactic or therapeutic treatment of a
 CC subject; an isolated modified cell comprising at least one first
 CC heterologous nucleic acid molecule, where the first heterologous nucleic
 CC acid molecule comprises a first polynucleotide sequence that encodes a
 CC first polypeptide; a non-human animal deficient in the polypeptide or
 CC that over-expresses the polypeptide; isolated tissues derived from the
 CC non-human animal; and one or more cells derived from the non-human
 CC animal. The nucleic acid is useful in preparing a composition for
 CC diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
 CC This is the amino acid sequence of a novel human polypeptide of the
 CC invention.
 XX
 SQ Sequence 1180 AA;

Query Match 84.2%; Score 32; DB 8; Length 1180;
 Best Local Similarity 71.4%; Pred. No. 2e+03;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WMLAAPS 7
 Db 746 WMLAAPS 752

RESULT 50
 ABG21342
 ID ABG21342 standard; protein; 1923 AA.

AC ABG21342;
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21333.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN W0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS85529.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

PS Claim 20; SEQ ID NO 51701; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantifying a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPD at
 CC ftp.wipo.int/pub/published_pot_sequences

XX
 SQ Sequence 1923 AA;

Query Match 84.2%; Score 32; DB 4; Length 1923;
 Best Local Similarity 71.4%; Pred. No. 3.3e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy	1	WMLSAFS	7
Db	208	WMLSAFS	214

Search completed: August 29, 2006, 05:59:27
Job time : 68.7426 secs

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OM protein - protein search, using sw model

Run on: August 29, 2006, 06:00:58 ; Search time 7 Seconds
(without alignments)
96.217 Million cell updates/sec

Title: US-10-541-343-3

Perfect score: 38

Sequence: 1 WMLSAFS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	637	2	A56263
2	32	84.2	187	2	T30536
3	32	84.2	280	2	C70696
4	32	84.2	345	2	AB1813
5	32	84.2	392	2	D83934
6	32	84.2	465	1	WZBBB4
7	31	81.6	149	2	D84181
8	31	81.6	187	2	T51719
9	31	81.6	257	2	H83697
10	31	81.6	265	2	T01568
11	31	81.6	365	2	E97674
12	31	81.6	368	2	AD2899
13	31	81.6	371	1	OPUG65
14	31	81.6	371	1	JC1268
15	31	81.6	372	1	OPUG3P
16	31	81.6	372	1	OPUGAP
17	31	81.6	372	1	OPUGBP
18	31	81.6	372	2	S01028
19	31	81.6	372	2	A36693
20	31	81.6	372	2	JT0402
21	31	81.6	372	2	A43638
22	31	81.6	372	2	S69246
23	31	81.6	372	2	B43638
24	31	81.6	372	2	A32322
25	31	81.6	372	2	US0065
26	31	81.6	372	2	B32332
27	31	81.6	372	2	JH0156
28	31	81.6	373	2	A27817
29	31	81.6	416	2	D96955

30	31	81.6	541	2	T48836	hypothetical prote
31	31	78.9	1121	2	C82120	transcription regu
32	30	78.9	182	2	B53189	cytochrome b560 ho
33	30	78.9	271	2	T11590	hypothetical prote
34	30	78.9	305	2	D96769	hypothetical prote
35	30	78.9	332	2	G64141	probable tetraacyl
36	30	78.9	341	2	C90322	glycosyltransferas
37	30	78.9	348	2	B97444	tetraacyldisacchar
38	30	78.9	348	2	AC2662	probable alpha-1,6
39	30	78.9	374	2	E82168	tyrosine-specific
40	30	78.9	400	2	D82419	glycoprotein antiq
41	30	78.9	401	2	S65138	p47 protein - pig
42	30	78.9	409	2	T11743	probable transmemb
43	30	78.9	412	2	F95394	probable metabolit
44	30	78.9	417	2	AC0546	PAS-6/7 protein pr
45	30	78.9	427	2	S74211	hypothetical prote
46	30	78.9	454	2	A75444	conserved hypochet
47	30	78.9	467	2	F90544	integral membrane
48	30	78.9	501	2	S70171	hypothetical prote
49	30	78.9	548	2	T40598	glutamate receptor
50	30	78.9	906	2	A39780	hypothetical prote
51	30	78.9	925	2	T01384	hypothetical prote
52	30	78.9	1321	2	T29308	hypothetical prote
53	30	78.9	1372	2	T29309	hypothetical prote
54	29	76.3	119	2	E95955	hypothetical prote
55	29	76.3	158	2	B82190	hypothetical prote
56	29	76.3	201	2	AD2503	hypothetical prote
57	29	76.3	220	2	S40931	hypothetical prote
58	29	76.3	252	2	F69955	probable ABC trans
59	29	76.3	279	2	C64620	hypothetical prote
60	29	76.3	279	2	B71894	hypothetical prote
61	29	76.3	279	2	S12864	retinal isomerase
62	29	76.3	301	1	S12864	citg protein - Kle
63	29	76.3	302	2	S60777	cathapsin L (EC 3.
64	29	76.3	313	2	S47433	cysteine proteinas
65	29	76.3	330	2	S19651	glycosyltransferas
66	29	76.3	339	2	H83252	hypothetical prote
67	29	76.3	347	2	D84649	hypothetical prote
68	29	76.3	350	2	T05149	NADH dehydrogenas
69	29	76.3	352	2	B34284	conserved hypochet
70	29	76.3	356	2	A11393	multidrug-efflux t
71	29	76.3	390	2	D69757	colicin V secretio
72	29	76.3	411	2	AB0013	probable esterase
73	29	76.3	413	1	IKC5A	alpha 2-adrenocept
74	29	76.3	431	2	H70731	two-component sens
75	29	76.3	432	2	I50829	hypothetical prote
76	29	76.3	446	2	T45358	hypothetical prote
77	29	76.3	446	2	C70783	hypothetical prote
78	29	76.3	450	2	T21515	hypothetical prote
79	29	76.3	479	2	T50726	hypothetical prote
80	29	76.3	514	2	S54019	extracellular solu
81	29	76.3	529	2	G75577	protein similar to
82	29	76.3	553	2	AC2931	ABC transporter AT
83	29	76.3	564	2	G86358	hypothetical prote
84	29	76.3	565	2	B86359	conserved hypochet
85	29	76.3	608	2	AD2000	ABC transporter at
86	29	76.3	611	2	T04510	hypothetical prote
87	29	76.3	630	2	C98351	oligopeptide-bind
88	29	76.3	641	2	AG2164	hypothetical prote
89	29	76.3	685	2	S65974	conserved hypochet
90	29	76.3	759	2	B90520	ABC transporter at
91	29	76.3	764	2	T22925	hypothetical prote
92	29	76.3	767	2	E96813	probable Oxidodqua
93	29	76.3	933	1	BVECC	sensor protein rcs
94	29	76.3	933	2	C91017	sensor for ctr cap
95	29	76.3	933	2	E85861	hypothetical prote
96	29	76.3	954	2	S60301	H+-exporting ATPas
97	29	76.3	954	2	H96838	hypothetical prote
98	29	76.3	1065	2	A70797	hypothetical prote
99	29	76.3	1151	2	T33777	hypothetical prote
100	29	76.3	1151	2	T42893	probable spectrin
101	29	76.3	4101	2	T32630	hypothetical prote
102	28	73.7	65	2	T36041	hypothetical prote

103	28	73.7	71	2	A64629	176	28	73.7	533	2	S18539	actva-1 protein -
104	28	73.7	71	2	D71885	177	28	73.7	550	2	A82378	conserved hypotet
105	28	73.7	79	2	AD3009	178	28	73.7	560	2	S46734	hypothetical prote
106	28	73.7	85	2	B98275	179	28	73.7	584	1	VCMS7A	env polypeptin pr
107	28	73.7	97	2	CG9841	180	28	73.7	616	2	E84424	probable auxin tra
108	28	73.7	104	2	F81814	181	28	73.7	647	2	T51808	probable auxin eft
109	28	73.7	137	2	D75337	182	28	73.7	663	2	T30621	hypothetical prote
110	28	73.7	153	2	CG9660	183	28	73.7	716	2	D69855	conserved hypotet
111	28	73.7	162	2	C32322	184	28	73.7	722	2	F87662	conserved hypotet
112	28	73.7	162	2	A10884	185	28	73.7	830	2	S50810	Feonb-dependent rec
113	28	73.7	162	2	B91113	186	28	73.7	843	2	A40970	undulin 1 - human
114	28	73.7	162	2	B85958	187	28	73.7	880	2	T02245	hypothetical prote
115	28	73.7	162	2	F65085	188	28	73.7	884	2	S55651	DNA helicase-prima
116	28	73.7	163	2	D64025	189	28	73.7	889	2	JC6015	chitin synthase (E
117	28	73.7	174	2	D91117	190	28	73.7	1061	2	D98008	conserved hypotet
118	28	73.7	188	2	S74963	191	28	73.7	1085	2	H82511	hypothetical prote
119	28	73.7	194	2	A11038	192	28	73.7	1085	2	S40476	Ca(2+)-sensing rec
120	28	73.7	207	2	S53801	193	28	73.7	1116	2	S41915	DNA-directed RNA p
121	28	73.7	209	2	B82388	194	28	73.7	1136	2	T40355	hypothetical prote
122	28	73.7	212	2	PS0012	195	28	73.7	1852	1	VJCH2	vitellogenin II pr
123	28	73.7	213	2	CG2953	196	28	73.7	4342	2	H83343	probable non-ribos
124	28	73.7	263	2	A21195	197	27	71.1	106	2	AB1987	hypothetical prote
125	28	73.7	266	2	JC7300	198	27	71.1	110	2	AC1958	hypothetical prote
126	28	73.7	267	2	JC4857	199	27	71.1	145	2	H69618	stres- and starva
127	28	73.7	288	2	S17659	200	27	71.1	148	2	E82925	hypothetical prote
128	28	73.7	291	2	B85018	201	27	71.1	148	2	E84023	hypothetical prote
129	28	73.7	299	2	B82504	202	27	71.1	162	2	F84119	ATP synthase subun
130	28	73.7	302	2	CG6531	203	27	71.1	166	2	AG3566	hypothetical prote
131	28	73.7	305	2	T52111	204	27	71.1	174	2	F83514	conserved hypotet
132	28	73.7	305	2	B84848	205	27	71.1	176	1	F64864	protein-disulfide
133	28	73.7	307	2	T52109	206	27	71.1	176	2	AH0723	disulfide bond for
134	28	73.7	308	2	T46026	207	27	71.1	176	2	H85696	hypothetical prote
135	28	73.7	311	2	CG4719	208	27	71.1	176	2	H90838	protein-disulfide
136	28	73.7	313	2	T11272	209	27	71.1	177	1	CG4067	probable protein-d
137	28	73.7	315	2	AB1812	210	27	71.1	195	2	S24997	formate C-acetyltr
138	28	73.7	315	2	T50562	211	27	71.1	199	2	T48763	hypothetical prote
139	28	73.7	315	2	T50561	212	27	71.1	219	2	A70314	deoxyribose-phosph
140	28	73.7	318	2	T20063	213	27	71.1	227	2	B37206	class II histocomp
141	28	73.7	321	2	T29419	214	27	71.1	227	2	A47635	MHC class II histo
142	28	73.7	326	2	AE1169	215	27	71.1	234	1	JH0529	tumor necrosis fac
143	28	73.7	335	2	A10295	216	27	71.1	265	2	E84533	hypothetical prote
144	28	73.7	345	2	T12347	217	27	71.1	265	2	T46952	probable membrane
145	28	73.7	347	2	H69867	218	27	71.1	266	2	AF1617	hypothetical prote
146	28	73.7	357	2	AD1769	219	27	71.1	266	2	AH1254	hypothetical prote
147	28	73.7	357	2	SS9531	220	27	71.1	274	1	A41461	fibronectin-bindin
148	28	73.7	372	1	OPJG2	221	27	71.1	277	2	T31855	hypothetical prote
149	28	73.7	383	2	T01706	222	27	71.1	280	2	H69288	conserved hypotet
150	28	73.7	383	2	H90482	223	27	71.1	282	2	T50040	capsular polysacch
151	28	73.7	385	2	S68780	224	27	71.1	290	2	E72676	hypothetical prote
152	28	73.7	387	2	B83553	225	27	71.1	292	2	G97310	dehydrogenase rela
153	28	73.7	395	2	B96610	226	27	71.1	305	1	CRHU5	carbonate dehydrat
154	28	73.7	400	2	C70082	227	27	71.1	314	2	G97050	DNA-methyltransfer
155	28	73.7	404	2	H83249	228	27	71.1	315	2	T47971	seven in absentia-
156	28	73.7	408	2	B84591	229	27	71.1	320	2	T27372	hypothetical prote
157	28	73.7	413	2	B83180	230	27	71.1	322	2	S45000	movement protein -
158	28	73.7	426	2	T32206	231	27	71.1	324	2	B71655	ribonucleoside-dip
159	28	73.7	429	2	B84410	232	27	71.1	327	2	T09027	hypothetical prote
160	28	73.7	429	2	T08562	233	27	71.1	328	2	C97781	hypothetical prote
161	28	73.7	439	2	B75487	234	27	71.1	330	2	C82777	DNA polymerase III
162	28	73.7	440	2	F83235	235	27	71.1	334	2	B81406	probable integral
163	28	73.7	440	2	S11793	236	27	71.1	335	2	E84992	tryptophan-tRNA li
164	28	73.7	442	2	T16773	237	27	71.1	336	2	T50560	SIN1A1 protein [im
165	28	73.7	449	2	D85962	238	27	71.1	340	2	B86363	hypothetical prote
166	28	73.7	449	2	H65089	239	27	71.1	350	2	T25156	hypothetical prote
167	28	73.7	466	2	H81697	240	27	71.1	364	2	T25155	hypothetical prote
168	28	73.7	466	2	G71542	241	27	71.1	374	2	T33173	hypothetical prote
169	28	73.7	469	2	D70048	242	27	71.1	388	2	G90450	hypothetical prote
170	28	73.7	483	2	F81221	243	27	71.1	393	2	S49759	probable membrane
171	28	73.7	490	2	S77201	244	27	71.1	397	2	C84078	porin O precursor
172	28	73.7	494	2	H81992	245	27	71.1	398	2	A82820	hypothetical prote
173	28	73.7	511	2	S44275	246	27	71.1	399	2	T21586	hypothetical prote
174	28	73.7	513	2	S63701	247	27	71.1	399	2	T27853	hypothetical prote
175	28	73.7	521	2	D96992	248	27	71.1	417	2	T34561	hypothetical prote

249	27	71.1	423	2	D89949	322	27	71.1	1703	2	S15047	SNF2 protein - yea
250	27	71.1	435	2	S78258	323	27	71.1	1784	2	T02844	cdcl6-related prot
251	27	71.1	426	2	T22568	324	27	71.1	1905	2	T18267	multidrug resistan
252	27	71.1	431	2	A95419	325	27	71.1	1845	2	T18402	asparagine/asparta
253	27	71.1	434	2	AF0883	326	27	71.1	3844	2	S28600	apollipoprotein C-I
254	27	71.1	438	2	T39268	327	27	71.1	4085	2	S13188	apollipoprotein C-I
255	27	71.1	440	1	RGEUC	328	26	68.4	66	2	H97817	hypothetical prote
256	27	71.1	440	2	R66050	329	26	68.4	72	1	M5Wt6B	E5b protein - huma
257	27	71.1	440	2	D91204	330	26	68.4	72	2	D61055	E5b protein - huma
258	27	71.1	443	2	AG0487	331	26	68.4	90	1	VKL0BR	trans-regulatory s
259	27	71.1	444	2	AD0238	332	26	68.4	91	2	T08665	hypothetical prote
260	27	71.1	450	2	T40446	333	26	68.4	94	2	T15982	hypothetical prote
261	27	71.1	457	2	T47005	334	26	68.4	97	2	C64022	hypothetical prote
262	27	71.1	459	2	F70884	335	26	68.4	97	2	T16463	hypothetical prote
263	27	71.1	471	2	AE0838	336	26	68.4	100	2	B28487	apollipoprotein C-I
264	27	71.1	483	2	A11908	337	26	68.4	108	2	T29281	hypothetical prote
265	27	71.1	493	2	T48630	338	26	68.4	113	2	AF1118	hypothetical prote
266	27	71.1	500	2	S49302	339	26	68.4	113	2	AH1478	hypothetical prote
267	27	71.1	502	2	C65263	340	26	68.4	122	2	AB2199	hypothetical prote
268	27	71.1	503	2	B84007	341	26	68.4	124	2	S60044	early nodulin 5 -
269	27	71.1	509	1	OAR1LO	342	26	68.4	135	2	F86756	prophage pi2 prote
270	27	71.1	509	2	S47553	343	26	68.4	137	2	D86768	hypothetical prote
271	27	71.1	529	2	T23190	344	26	68.4	139	2	G70464	chlorodoxin - Aqu
272	27	71.1	537	2	T38015	345	26	68.4	141	2	D87317	hypothetical prote
273	27	71.1	575	2	S50962	346	26	68.4	146	2	B83777	stresses- and starva
274	27	71.1	577	2	A53202	347	26	68.4	148	2	S76508	hypothetical prote
275	27	71.1	583	2	G84629	348	26	68.4	152	2	A10726	probable membrane
276	27	71.1	595	2	B64460	349	26	68.4	152	2	D64943	probable membrane
277	27	71.1	610	2	A84417	350	26	68.4	152	2	B99945	hypothetical prote
278	27	71.1	610	2	D83656	351	26	68.4	152	2	E85793	hypothetical prote
279	27	71.1	633	2	S76749	352	26	68.4	156	2	D75536	ribosomal protein
280	27	71.1	635	2	T41367	353	26	68.4	156	2	AE1550	non-heme iron-bind
281	27	71.1	643	2	S17997	354	26	68.4	156	2	B82359	DPS family protein
282	27	71.1	677	2	T08943	355	26	68.4	156	2	AG1192	non-heme iron-bind
283	27	71.1	679	2	G83492	356	26	68.4	157	2	S31634	hypothetical prote
284	27	71.1	701	2	C84972	357	26	68.4	157	2	T22831	hypothetical prote
285	27	71.1	706	2	AD0173	358	26	68.4	168	2	E95036	hypothetical prote
286	27	71.1	794	2	T23048	359	26	68.4	173	2	G87383	acetyltransferase,
287	27	71.1	918	2	S45872	360	26	68.4	179	2	A11863	hypothetical prote
288	27	71.1	940	2	T48700	361	26	68.4	179	2	JU0184	hypothetical 20.2K
289	27	71.1	1097	2	S17308	362	26	68.4	194	2	T29062	probable transcript
290	27	71.1	1164	2	S46769	363	26	68.4	195	2	D82313	2-amino-4-hydroxy-
291	27	71.1	1179	2	T05673	364	26	68.4	206	2	AB0786	probable membrane
292	27	71.1	1245	2	G84897	365	26	68.4	207	2	AC2069	acyl carrier prote
293	27	71.1	1257	2	T28937	366	26	68.4	208	2	AD2213	hypothetical prote
294	27	71.1	1341	2	T18301	367	26	68.4	212	2	S75535	hypothetical prote
295	27	71.1	1354	2	T18375	368	26	68.4	214	2	E82679	chaperone XF1452 {
296	27	71.1	1356	2	T18367	369	26	68.4	214	2	S06455	avenin precursor {
297	27	71.1	1368	2	T18379	370	26	68.4	224	2	AD0743	probable membrane
298	27	71.1	1379	2	T13718	371	26	68.4	224	2	C86192	protein T20W3.4 [i
299	27	71.1	1384	2	T18366	372	26	68.4	227	2	I61843	cytochrome-c oxida
300	27	71.1	1397	2	T18377	373	26	68.4	228	2	S75228	hypothetical prote
301	27	71.1	1399	2	T18370	374	26	68.4	232	2	AG1843	transcription regu
302	27	71.1	1407	2	T18381	375	26	68.4	232	2	E75559	hypothetical prote
303	27	71.1	1412	2	T18380	376	26	68.4	232	2	G89025	protein F13A2.8 [i
304	27	71.1	1420	2	T18385	377	26	68.4	235	2	E95876	conserved N1/Fe-hy
305	27	71.1	1420	2	T17158	378	26	68.4	243	2	AF0721	probable N1/Fe-hy
306	27	71.1	1422	2	T18383	379	26	68.4	251	2	PC4261	activin type II re
307	27	71.1	1433	2	A46053	380	26	68.4	253	2	AE2797	cytochrome C-type
308	27	71.1	1435	2	T18387	381	26	68.4	254	2	T36161	hypothetical prote
309	27	71.1	1435	2	T46611	382	26	68.4	255	2	AF3557	transcription regu
310	27	71.1	1439	2	T02087	383	26	68.4	257	2	E89124	protein K07C11.1 [
311	27	71.1	1450	2	T18382	384	26	68.4	261	2	T32399	hypothetical prote
312	27	71.1	1452	2	T17157	385	26	68.4	261	2	F96508	protein F27F5.3 [i
313	27	71.1	1463	2	T18386	386	26	68.4	265	2	G81241	capsule polysaccha
314	27	71.1	1463	2	T17159	387	26	68.4	265	2	S15222	ctrc protein - Nei
315	27	71.1	1465	2	T18384	388	26	68.4	266	2	A86288	protein F9U1.30 [i
316	27	71.1	1467	2	T17150	389	26	68.4	267	2	E97576	cytochrome C-type
317	27	71.1	1468	2	T05672	390	26	68.4	272	2	T01144	probable acetone-c
318	27	71.1	1478	2	T18388	391	26	68.4	278	2	AG2943	hypothetical prote
319	27	71.1	1478	2	T17185	392	26	68.4	278	2	A83430	transcription regu
320	27	71.1	1487	2	T14324	393	26	68.4	281	2	T26244	hypothetical prote
321	27	71.1	1680	2	T41628	394	26	68.4	285	2	C98339	hypothetical prote

395	26	68.4	286	2	D64235	hypothetical prote
396	26	68.4	287	2	T39197	yeast atp12 protei
397	26	68.4	289	2	B69217	hypothetical prote
398	26	68.4	290	2	T27891	hypothetical prote
399	26	68.4	292	2	A84935	5,10-methylener
400	26	68.4	297	2	D95964	probable transcrip
401	26	68.4	298	2	T36900	probable integral
402	26	68.4	298	2	T27365	hypothetical prote
403	26	68.4	298	2	C41047	exoenzyme S synth
404	26	68.4	299	2	B95939	probable spermidin
405	26	68.4	302	2	AC3020	GDEF family prote
406	26	68.4	302	2	P98264	hypothetical prote
407	26	68.4	308	2	T28943	hypothetical prote
408	26	68.4	309	2	AC3257	integrase/recombin
409	26	68.4	311	2	T50283	hypothetical trans
410	26	68.4	314	2	T46743	carbamate kinase (
411	26	68.4	314	2	S68783	carbamate kinase (
412	26	68.4	315	2	T11388	cathepsin L (EC 3.
413	26	68.4	315	2	H86836	NADH2 dehydrogen
414	26	68.4	315	2	T28942	carbamate kinase (
415	26	68.4	317	2	T24346	hypothetical prote
416	26	68.4	318	2	D69742	hypothetical prote
417	26	68.4	319	2	B81382	hypothetical prote
418	26	68.4	319	2	S44746	tryptophan-cRNA li
419	26	68.4	320	2	T23635	CotD8.1 protein -
420	26	68.4	320	2	T25308	hypothetical prote
421	26	68.4	322	2	B84908	hypothetical prote
422	26	68.4	324	1	A48953	choloyleglycine hyd
423	26	68.4	324	2	T28940	hypothetical prote
424	26	68.4	325	2	AC2053	hypothetical prote
425	26	68.4	326	2	AB3100	hypothetical prote
426	26	68.4	326	2	H98186	probable mikimopin
427	26	68.4	328	2	AE9425	iron (III) ABC tra
428	26	68.4	329	2	H83604	hypothetical prote
429	26	68.4	333	2	T02690	hypothetical prote
430	26	68.4	338	2	FE9035	conserved hypotet
431	26	68.4	340	2	S54821	cbrB protein - Brw
432	26	68.4	341	2	T40424	hypothetical prote
433	26	68.4	343	2	D75370	hypothetical prote
434	26	68.4	344	2	B90564	potassium channel
435	26	68.4	344	2	AF3626	nickel resistance
436	26	68.4	346	2	A02991	ABC transporter, m
437	26	68.4	346	2	B98292	ribose ABC transpo
438	26	68.4	346	2	T24178	hypothetical prote
439	26	68.4	347	2	A95341	probable hydrolase
440	26	68.4	349	2	I59336	galatin receptor 1
441	26	68.4	354	2	AF1051	conserved hypotet
442	26	68.4	355	2	H82481	conserved hypotet
443	26	68.4	356	2	H84934	UDP-N-acetylmutam
444	26	68.4	356	2	H86115	hypothetical prote
445	26	68.4	356	2	S56417	hypothetical 40.3K
446	26	68.4	356	2	H91274	hypothetical prote
447	26	68.4	357	2	AF2207	hypothetical prote
448	26	68.4	364	2	UC4249	reEP protein - Az
449	26	68.4	365	2	S27268	activin receptor S
450	26	68.4	366	2	A13342	D-alanine-D-alanin
451	26	68.4	368	2	F75546	conserved hypotet
452	26	68.4	368	2	S18758	hypothetical prote
453	26	68.4	370	2	T27197	hypothetical prote
454	26	68.4	375	2	I19169	slslyltransferase
455	26	68.4	375	2	I48686	N-glycan alpha 2,8
456	26	68.4	378	2	A46727	slslyltransferase
457	26	68.4	378	2	A55735	G protein-couple
458	26	68.4	382	2	B49193	type II activin re
459	26	68.4	384	2	T49084	hypothetical prote
460	26	68.4	395	2	F97023	aspartate aminotra
461	26	68.4	397	2	D72220	probable aspartate
462	26	68.4	398	2	T38298	WD repeat protei
463	26	68.4	400	2	AF0291	multidrug resist
464	26	68.4	403	2	C83825	hypothetical prote
465	26	68.4	404	2	D82968	conserved hypotet
466	26	68.4	406	2	C75537	hypothetical prote
467	26	68.4	409	2	A84602	

468	26	68.4	412	2	G64059	probable serine tr
469	26	68.4	413	2	B64536	serine transport p
470	26	68.4	417	2	D82172	serine transporter
471	26	68.4	421	2	F83852	glutamate dehydrog
472	26	68.4	422	2	S73369	hypothetical prote
473	26	68.4	428	2	A55044	beta-4C-adrenergic
474	26	68.4	431	2	T24941	hypothetical prote
475	26	68.4	432	2	F96919	ABC transporter (p
476	26	68.4	433	2	AB3273	ammonium transport
477	26	68.4	435	1	S18609	glutamate dehydrog
478	26	68.4	435	2	AC0104	probable sugar tra
479	26	68.4	436	2	UC4841	regeneration assoc
480	26	68.4	439	2	G70693	probable dnf prot
481	26	68.4	440	2	T20092	hypothetical prote
482	26	68.4	440	2	G96600	protein F14J16.24
483	26	68.4	443	2	B39794	transcription fact
484	26	68.4	444	2	A39794	transcription fact
485	26	68.4	444	2	B36389	transcription fact
486	26	68.4	445	2	D82328	probable Na+/H+ an
487	26	68.4	446	2	S77010	nickel resistance
488	26	68.4	446	2	T19625	hypothetical prote
489	26	68.4	447	2	T09414	pectinesterase hom
490	26	68.4	450	1	S13730	pmba protein - Esc
491	26	68.4	450	2	F82402	permease VCA0904 (
492	26	68.4	450	2	D86121	maturation of anti
493	26	68.4	450	2	D91280	maturation of anti
494	26	68.4	452	1	G70064	transporter homolo
495	26	68.4	457	2	AD3073	hypothetical prote
496	26	68.4	457	2	B98213	hypothetical prote
497	26	68.4	460	2	D72694	hypothetical prote
498	26	68.4	463	2	T39929	thiamin-repressibl
499	26	68.4	469	2	B82264	probable polysacch
500	26	68.4	473	2	AE0801	probable amino aci

ALIGNMENTS

RESULT 1

A56263 beta-galactosidase (EC 3.2.1.23) isozyme 12 - Arthrobacter sp. (strain B7)

C:Species: Arthrobacter sp.

C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 16-Aug-2004

C:Accession: A56263

R:Guthrie, K.R.; Trimbur, D.E.; Kasim, J.J.; Brenchley, J.D.

J. Bacteriol. 177, 1981-1988, 1995

A:Title: Analysis of a novel gene and beta-galactosidase isozyme from a psychrotrophic Ar

A:Reference number: A56263; MUID:95238267; PMID:7721689

A:Accession: A56263

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: UNIPARC:U010000856E1; GB:U17417; NID:ig676845; PID:AAA75601.1; PID:

C:Superfamily: beta-galactosidase, Bgal type

C:Keywords: glycosidase; hydrolase

Query March 89.5%; Score 34; DB 2; Length 637;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 372 WMLSCFS 378

RESULT 2

T30536 hypothetical protein 2 - Fugu rubripes (fragment)

C:Species: Fugu rubripes

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C:Accession: T30536

R:Riboldi Tumaciliffe, G.R.; Platzer, M.; Nyakatura, G.; Elgar, G.S.; Brenner, S.; Rosent

submitted to the EMBL Data Library, September 1997

A;Description: Analysis of the genomic loci of Fugu rubripes homologs of the human disea
A;Reference number: Z20848
A;Accession: T30536
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-187 <RTB>
A;Cross-references: UNIPROT:O73698; UNIPARC:UPI00001B8E6; EMBL:AF026198; NID:g3098263;
C;Genetics:
A;Note: PUT2
A;Note: Intron positions not resolved (incomplete sequence)

Query Match 84.2%; Score 32; DB 2; Length 187;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 9 WMLAFA 15

RESULT 3
C70696
probable transport system permease - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: C70696
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
R;Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70696
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-280 <COL>
A;Cross-references: UNIPROT:P72049; UNIPARC:UPI00000D1237; GB:Z80343; GB:AL123456; NID:9
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV3783
C;Superfamily: Integral membrane O-antigen translocator protein rfbA

Query Match 84.2%; Score 32; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 262 WMLAFA 268

RESULT 4
AB1813
hypothetical protein all0050 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB1813
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasa moto, S.; Watanabe, A.; Iri guchi
Nakazaki, N.; Shimp o, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB1813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <KTB>
A;Cross-references: UNIPROT:Q820P0; UNIPARC:UPI00000CDBF9; GB:BA000019; PIDN:BA877574.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0050

Query Match 84.2%; Score 32; DB 2; Length 345;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 29 WMLSSFS 35

RESULT 5
D83934
hypothetical protein BH2276 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83934
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83934
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <STO>
A;Cross-references: UNIPROT:Q9KAL1; UNIPARC:UPI00000C3E6F; GB:AP001515; GB:BA000004; NID
C;Genetics:
A;Gene: BH2276

Query Match 84.2%; Score 32; DB 2; Length 392;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 347 WMLQAFS 353

RESULT 6
WZBBB4
51.3K capsid protein - equine herpesvirus 1 (strain Ab4p)
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: E36797
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Submitted to Genbank, March 1992
A;Description: The DNA sequence of equine herpesvirus-1.
A;Reference number: A36805
A;Accession: E36797
A;Molecule type: DNA
A;Residues: 1-465 <TEL>
A;Cross-references: UNIPROT:P28935; UNIPARC:UPI000013B9A; GB:M86664; NID:g330791; PIDN:
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:9228556; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Genetics:
A;Gene: 22
C;Superfamily: varicella-zoster virus gene 20 protein
C;Keywords: capsid assembly; capsid protein

Query Match 84.2%; Score 32; DB 1; Length 465;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 99 WMLSSFN 105

RESULT 7

D84181
hypothetical protein Vng0208h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: D84181
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leitbauer, B.; Keller, K.; Cruz, R.; Danon, M.D.; Hough, D.W.; Maddocks, D.G.; Jaldic
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: D84181
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-149 <STD>
A/Cross-references: UNIPROT:Q9H818; UNIPARC:UPI0000063597; GB:AE004437; NID:g10579852; F
C/Genetics:
A/Gene: VNG0208H

Query Match 81.6%; Score 31; DB 2; Length 149;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 88 WMLDSFS 94

RESULT 8
T51719
hypothetical protein [imported] - Streptococcus mutans
C:Species: Streptococcus mutans
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C/Accession: T51719
R:Boyd, D.A.; Thevenot, T.; Gumbmann, M.; Honeyman, A.L.; Hamilton, I.R.
Infect. Immun. 68, 925-930, 2000
A:Title: Identification of the operon for the sorbitol (glucitol) phosphoenolpyruvate su
A:Reference number: 225439; MUID:20107103; PMID:10639465
A/Accession: T51719
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-187 <BOY>
A/Cross-references: UNIPROT:Q9X669; UNIPARC:UPI00000DCB3B; EMBL:AF132127; PIDN:AMD33516.
A/Experimental source: strain LT11

Query Match 81.6%; Score 31; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 10 WMLSAF 15

RESULT 9
H83697
hypothetical protein BH0384 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: H83697
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: H83697
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-257 <STD>
A/Cross-references: UNIPROT:Q9KFU2; UNIPARC:UPI00000C386B; GB:AP001508; GB:BA000004; NID
C/Genetics:
A/Experimental source: strain C-125
A/Gene: BH0384

Query Match 81.6%; Score 31; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 183 WMLSAF 188

RESULT 10
T01568
hypothetical protein A_TM018A10.12 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01568
R:Dempsey, S.; Harper, M.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of A. thaliana TM018A10.
A:Reference number: Z14348
A/Accession: T01568
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-265 <DEM>
A/Cross-references: UNIPROT:Q23098; UNIPARC:UPI00000A37E8; EMBL:AF013294; NID:g2252848; I
C/Genetics:
A/Experimental source: cultivar Columbia
A/Map position: 4
A:Introns: 43/2; 92/1; 186/2
A>Note: AA_TM018A10.12
C:Superfamily: Arabidopsis thaliana hypothetical protein A_TM018A10.12

Query Match 81.6%; Score 31; DB 2; Length 265;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 160 WMLSKFS 166

RESULT 11
E97674
hypothetical protein AGR_C_4767 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: E97674
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:2160851; PMID:11743194
A/Accession: E97674
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-365 <KUR>
A/Cross-references: UNIPROT:Q8U533; UNIPARC:UPI00000D28EF; GB:AE007869; PIDN:AAK88350.1;
C/Genetics:
A/Gene: AGR_C_4767
A/Map position: circular chromosome

Query Match 81.6%; Score 31; DB 2; Length 365;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 195 WMLSSF 200

RESULT 12
AD2899
conserved hypothetical protein Atu2629 [imported] - Agrobacterium tumefaciens (strain C5

C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD2899
R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2899
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <KOR>
A:Cross-references: UNIPROT:Q8UC69; UNIPARC:UPI00000D1F84; GB:AE008688; P1DN:AA43610.1;
C:Genetics:
A:Gene: Atu2629
A:Map position: circular chromosome

Query Match 81.6%; Score 31; DB 2; Length 368;
Best Local Similarity 83.3%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 198 WMLSSF 203

RESULT 13
ORU65
diarylpropane peroxidase (EC 1.11.1.14) H10 precursor - basidiomycete (Phanerochaete chr
N:Alternate names: diarylpropane oxygenase; lignin peroxidase GLG5; Ligninase
C:Species: Phanerochaete chrysosporium
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 12-Jul-2004
C:Accession: JN0117; S13565; E29610; E60995
R:Zhang, Y.Z.; Reddy, C.A.; Rasooly, A.
Gene 97, 191-198, 1991
A:Title: Cloning of several lignin peroxidase (lup)-encoding genes: sequence analysis of
A:Reference number: JN0117; MUID:91153647; PMID:1999283
A:Accession: JN0117
A:Molecule type: DNA
A:Residues: 1-371 <ZHA>
A:Cross-references: UNIPROT:P1543; UNIPARC:UPI000004CB03; GB:M63496; EMBL:M36815; NID:G
A:Experimental source: strain BKMFI767; ATCC 24725
R:Gaskell, J.; Dieperink, E.; Cullen, D.
Nucleic Acids Res. 19, 599-603, 1991
A:Title: Genomic organization of lignin peroxidase genes of Phanerochaete chrysosporium.
A:Reference number: S13563; MUID:91187681; PMID:2011531
A:Accession: S13565
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-371 <GAS>
A:Cross-references: UNIPARC:UPI000004CB03; GB:X55343; EMBL:X54256; NID:g3137; P1DN:CAA35
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1990
R:de Boer, H.A.; Zhang, Y.Z.; Collins, C.; Reddy, C.A.
Gene 60, 93-102, 1987
A:Title: Analysis of nucleotide sequences of two ligninase cDNAs from a white-rot fungus
A:Reference number: A91587; MUID:8815506; PMID:3440521
A:Accession: B29610
A:Molecule type: mRNA
A:Residues: 1-371 <DEB>
A:Cross-references: UNIPARC:UPI000004CB03; GB:M18743
R:Dass, S.B.; Reddy, C.A.
FEMS Microbiol. Lett. 69, 221-224, 1990
A:Title: Characterization of extracellular peroxidases produced by acetate-buffered cult
A:Reference number: A60995
A:Accession: B60995
A:Molecule type: protein
A:Residues: 28-37 <DAS>
A:Cross-references: UNIPARC:UPI00001721E6
A:Experimental source: ATCC 24725

C:Comment: Lignin peroxidases play a key role in the initial depolymerization and degrad
C:Genetics:
A:Gene: GLG5; LIP6
A:Insertions: 21/3; 71/2; 90/1; 161/1; 175/1; 201/2; 243/2; 343/3; 365/2
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-27/Domain: propeptide #status predicted <PRO>
F:28-371/Product: lignin peroxidase H10 #status experimental <MAT>
F:283/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.6%; Score 31; DB 1; Length 371;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 197 WMLSAHS 203

RESULT 14
JC1268
lignin peroxidase (EC 1.11.1.-) 2 precursor - basidiomycete (Phanerochaete chrysosporium)
N:Alternate names: lignin peroxidase H6; Ligninase H6
C:Species: Phanerochaete chrysosporium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 12-Jul-2004
C:Accession: JC1268; JH0491; PS0247; C60995
R:Ritch Jr., T.G.; Gold, M.H.
Gene 118, 73-80, 1992
A:Title: Characterization of a highly expressed lignin peroxidase-encoding gene from the
A:Reference number: JC1268; MUID:92380494; PMID:1511887
A:Accession: JC1268
A:Molecule type: DNA
A:Residues: 1-371 <RT>
A:Cross-references: UNIPROT:P49012; UNIPARC:UPI000012B681; GB:M92644; NID:g169277; P1DN:
A:Experimental source: strain OGCI01
R:Ritch Jr., T.G.; Nipper, V.J.; Akileswaran, L.; Smith, A.J.; Pribnow, D.G.; Gold, M.H.
Gene 107, 119-126, 1991
A:Title: Lignin peroxidase from the basidiomycete Phanerochaete chrysosporium is synthe
A:Reference number: JH0491; MUID:92077421; PMID:1743510
A:Accession: JH0491
A:Molecule type: mRNA
A:Residues: 1-371 <RT2>
A:Cross-references: UNIPARC:UPI000012B681; GB:M74229; NID:g169271; P1DN:AAA33735.1; P1D:
A:Experimental source: strain OGCI01
A:Accession: PS0247
A:Molecule type: protein
A:Residues: 29-48 <RT1>
A:Cross-references: UNIPARC:UPI0000175214
R:Dass, S.B.; Reddy, C.A.
FEMS Microbiol. Lett. 69, 221-224, 1990
A:Title: Characterization of extracellular peroxidases produced by acetate-buffered cult
A:Reference number: A60995
A:Accession: C60995
A:Molecule type: protein
A:Residues: 28-38 <DAS>
A:Cross-references: UNIPARC:UPI0000175215
A:Experimental source: ATCC 24725
C:Comment: Lignin peroxidase is one of the major components of the lignin degradative sy
C:Genetics:
A:Gene: LGS2
A:Insertions: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-28/Domain: propeptide #status predicted <PRO>
F:29-371/Product: lignin peroxidase #status predicted <MAT>
F:295/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.6%; Score 31; DB 2; Length 371;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 Db 199 WMLSAHS 205

RESULT 15

OPUGBP

lignin peroxidase (EC 1.11.1.-) GLG3 precursor - basidiomycete (Phanerochaete chrysosporium)
 N:Alternate names: ligninase LIP4
 C:Species: Phanerochaete chrysosporium
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 12-Jul-2004
 C:Accession: S13723
 R:Naidu, P.S.; Reddy, C.A.
 Nucleic Acids Res. 18, 7173, 1990
 A:Title: Nucleotide sequence of a new lignin peroxidase gene GLG3 from the white-rot fungus
 A:Reference number: S13723; MUID:91088334; PMID:2129560
 A:Accession: S13723
 A:Molecule type: DNA
 A:Residues: 1-372 <NMI>
 A:Cross-references: UNIPROT:P21764; UNIPARC:UPI0000126682; EMBL:X51590; NID:g3135; PIDN:
 A>Note: the authors translated the codon CAG for residue 5 as Glu
 C:Genetics:
 A:Gene: GLG3
 A:Introns: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
 C:Superfamily: peroxidase
 C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-372/Product: lignin peroxidase GLG3 #status predicted <MAT>
 F:285/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 81.6%; Score 31; DB 1; Length 372;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 Db 199 WMLSAHS 205

RESULT 16

OPUGBP

lignin peroxidase (EC 1.11.1.-) LIP4 precursor - basidiomycete (Phanerochaete chrysosporium)
 N:Alternate names: ligninase LIP4
 C:Species: Phanerochaete chrysosporium
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 12-Jul-2004
 C:Accession: S13563
 R:Gaskell, J.; Dieperink, E.; Cullen, D.
 Nucleic Acids Res. 19, 599-603, 1991
 A:Title: Genomic organization of lignin peroxidase genes of Phanerochaete chrysosporium.
 A:Reference number: S13563; MUID:91187681; PMID:2011531
 A:Accession: S13563
 A:Molecule type: DNA
 A:Residues: 1-372 <GAS>
 A:Cross-references: UNIPROT:P31837; UNIPARC:UPI0000126687; EMBL:X54257; NID:g3154; PIDN:
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1990
 C:Genetics:
 A:Gene: LIP4
 A:Introns: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
 C:Superfamily: peroxidase
 C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-372/Product: lignin peroxidase LIP4 #status predicted <MAT>
 F:285/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 81.6%; Score 31; DB 1; Length 372;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 Db 199 WMLSAHS 205

RESULT 17

OPUGBP

lignin peroxidase (EC 1.11.1.-) LIPB precursor - basidiomycete (Phanerochaete chrysosporium)
 N:Alternate names: ligninase LIP4
 C:Species: Phanerochaete chrysosporium
 C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 12-Jul-2004
 C:Accession: S13564
 R:Gaskell, J.; Dieperink, E.; Cullen, D.
 Nucleic Acids Res. 19, 599-603, 1991
 A:Title: Genomic organization of lignin peroxidase genes of Phanerochaete chrysosporium.
 A:Reference number: S13563; MUID:91187681; PMID:2011531
 A:Accession: S13564
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-372 <GAS>
 A:Cross-references: UNIPROT:P3183; UNIPARC:UPI0000126689; EMBL:X54257; NID:g3154; PIDN:
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1990
 C:Genetics:
 A:Gene: LIPB
 A:Introns: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
 C:Superfamily: peroxidase
 C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-372/Product: lignin peroxidase LIPB #status predicted <MAT>
 F:285/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 81.6%; Score 31; DB 1; Length 372;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 Db 199 WMLSAHS 205

RESULT 18

S01028

lignin peroxidase (EC 1.11.1.-) LPOA precursor - basidiomycete (Phanerochaete chrysosporium)
 N:Alternate names: lignin peroxidase H8; ligninase H8
 C:Species: Phanerochaete chrysosporium
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 12-Jul-2004
 C:Accession: S01028
 R:Smith, T.V.; Schnalch, H.; Gaskell, J.; Covert, S.; Cullen, D.
 Nucleic Acids Res. 16, 1219, 1988
 A:Title: Nucleotide sequence of a ligninase gene from Phanerochaete chrysosporium.
 A:Reference number: S01028; MUID:88144011; PMID:3344218
 A:Accession: S01028
 A:Molecule type: DNA
 A:Residues: 1-372 <SMI>
 A:Cross-references: UNIPROT:P06181; UNIPARC:UPI0000166963; EMBL:X06689; NID:g3145; PIDN:
 A>Note: the authors translated the codon GAC for residue 213 as Asn
 C:Genetics:
 A:Gene: LPOA
 A:Introns: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
 C:Superfamily: peroxidase
 C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 81.6%; Score 31; DB 2; Length 372;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 |||||
 Db 199 WMLSAHS 205

RESULT 19

A36693

lignin peroxidase (EC 1.11.1.-) GLG6 precursor - basidiomycete (Phanerochaete chrysosporium)
 C:Species: Phanerochaete chrysosporium
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 12-Jul-2004
 C:Accession: A36693

R;Naidu, P.S.; Zhang, Y.Z.; Reddy, C.A.
Biochem. Biophys. Res. Commun. 173, 994-1000, 1990
A;Title: Characterization of a new lignin peroxidase gene (GLG6) from Phanerochaete chrysosporium
A;Reference number: A36693; MUID:91097609; PMID:2268360
A;Accession: A36693

Query Match	81.6%	Score 31;	DB 2;	Length 372;
Similarity	85.7%;	Pred. No. 80;		
Best Local				
Matches	6; Conservative	0; Mismatches	1; Indels	0; Gaps

QY	1	WMLSAFS	7
Db	199	WMLSAHS	205

RESULT 20

lignin peroxidase (EC 1.11.1.-) precursor - basidiomycete (Phanerochaete chrysosporium)
C/Species: Phanerochaete chrysosporium
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 12-Jul-2004
C/Accession: J00402
R/Walther, I.; Kaein, M.; Reiser, J.; Suter, F.; Fritzsche, B.; Salohimo, M.; Leisola,
Gene 70, 127-137, 1988
A/TITLE: Molecular analysis of a Phanerochaete chrysosporium lignin peroxidase gene.
/Reference number: J00402; MUID:89196904; PMID:3240864

Query Match	81.6%	Score 31;	DB 2;	Length 372;
Best Local Similarity	85.7%;	Pred.	No. 80;	
Matches 6; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;

Qy		1	WMLSAFS	7
Dd		199	WMLSAHS	205

RESULT 21

A43638
lignin peroxidase (EC 1.11.1.-) 48 precursor - basidiomycete (Phanerochaete chrysosporium)
C/Species: Phanerochaete chrysosporium
C/Date: 11-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 12-Jul-2004
C/Accession: A43638
R/Andrawis, A.; Pease, E.A.; Kuan, I.; Holzbaur, E.; Tien, M.
Biochem. Biophys. Res. Commun. 162, 673-680, 1989
A/Title: Characterization of two lignin peroxidase clones from Phanerochaete chrysosporium
A/Reference number: A43638, MUID:89334875; PMID:2474293
A/Accession: A43638
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-372 <AND>
A/Cross-references: UNIPARC:UPI0000168966; GB:M27884; NID:gl69283; PIDN:AB0798.1; PID
A/Note: the authors translated the codon TGC for residue 41 as Ser, and TCG for residue
C/Superfamily: peroxidase
C/Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match	81.6%	Score 31;	DB 2;	Length 372;
Best Local Similarity	85.7%	Pred. No. 80;		
Matches 6; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	WMLSAFS	7
Db	199	WMLSAHS	205

RESULT 22

lignin peroxidase (EC 1.11.1.-) H₃ precursor - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 12-Jul-2004
C:Accession: S69246
R:Schneider, H.; Barth, W.; Boehme, H.J.
Biol. Chem. Hoppe-seyler 377, 399-402, 1996
A:Title: Cloning and characterization of another lignin peroxidase gene from the white-rot
A:Reference number: S69246; MUID:96437179; PMID:8839887
A:Accession: S69246
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-372 <SCH>
A:Cross-references: UNIPARC:UPI000017522D
A:Experimental source: strain BKM-F 1767
C:Genetics:
A:Gene: 11P
C:Function:
A:Description: wood degradation; involved in depolymerization and degradation of lignins
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F:1-38/Domain: signal sequence #status Predicted <SIG>
F:129-372/Product: lignin peroxidase H₃ #status predicted <MAT>
F:1285/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	81.6%	Score 31	DB 2	Length 372
Best Local Similarity	85.7%	Pred. No	80	
Matches	6	Conservative	0	Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|||
Db 199 WMLSAHS 205

RESULT 23

B43638
 lignin peroxidase (EC 1.11.1.-) lambda ML-5 precursor - basidiomycete (Phanerochaete chr
 C/Species: Phanerochaete chrysosporium
 C/Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 12-Jul-2004
 C/Accession: B43638
 R/Andrews, A., Pease, E.A., Kuan, I., Holzbaur, E., Tien, M.
 Biochem. Biophys. Res. Commun. 162, 673-680, 1989
 A/Title: Characterization of two lignin peroxidase clones from Phanerochaete chrysospori
 A/Reference number: A43638; MUID:89334875; PMID:2474293
 A/Accession: B43638
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-372 <AND-
 A/Cross-references: UNIPROT:001775; UNIPARC:UP10000175213

Query Match	81.6%	Score 31, DB 2	Length 372;
Best Local Similarity	85.7%	Pred. No. 80;	
Matches 6; Conservative	0;	Mismatches 1; Indels	0; Gaps 0;

QY	1	WMLSAFS	7
Db	199	WMLSAHS	205

RESULT 24

A3232
 lignin peroxidase (EC 1.11.1.-) H8 precursor - basidiomycete (Phanerochaete chrysosporium
 N/Alternate names: ligninase H8
 C/Species: Phanerochaete chrysosporium
 C/Date: 27-Feb-1990 #sequence revision 31-Dec-1993 #ext change 12-Jul-2004

C:Accession: A32322; S66556; D60995
R:Schalch, H.; Gaskell, J.; Smith, T.L.; Cullen, D.
Mol. Cell. Biol. 9, 2743-2747, 1989
A:Title: Molecular cloning and sequences of ligin peroxidase genes of Phanerochaete chrysosporium
A:Reference number: A32322; MUID:89343994; PMID:2761543
A:Accession: A32322
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-372 <SCH>
A:Cross-references: UNIPARC:UPI0000175221; GB:M27400
A>Note: the authors translated the codon CAG for residue 110 as His, GAC for residue 191
R:Doyle, W.A.; Smith, A.T.
Biochem. J. 315, 15-19, 1996
A:Title: Expression of ligin peroxidase H8 in Escherichia coli: folding and activation
A:Reference number: S66556; MUID:96207556; PMID:8670100
A:Accession: S66556
A:Molecule type: protein
A:Residues: 22-30 <DOY>
A:Cross-references: UNIPARC:UPI0000175222
R:Dass, S.B.; Reddy, C.A.
FEBS Microbiol. Lett. 69, 221-224, 1990
A:Title: Characterization of extracellular peroxidases produced by acetate-buffered cultures
A:Reference number: A60995
A:Accession: D60995
A:Molecule type: protein
A:Residues: 29-38 <DAS>
A:Cross-references: UNIPARC:UPI0000175223
A:Experimental source: ATCC 24725
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 81.6%; Score 31; DB 2; Length 372;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 199 WMLSAHS 205

RESULT 25
J50065
lignin peroxidase (EC 1.11.1.-) 1 precursor - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Jul-2004
C:Accession: J50065
R:Brown, A.; Sims, P.F.G.; Raeder, U.; Broda, P.
Gene 73, 77-85, 1988
A:Title: Multiple liginase-related genes from Phanerochaete chrysosporium.
A:Reference number: J50065; MUID:89211962; PMID:2907500
A:Accession: J50065
A:Molecule type: DNA
A:Residues: 1-372 <BRO>
A:Cross-references: UNIPROT:O01775; UNIPARC:UPI00006A835; GB:M24082; NID:G598354; PIDN:G598354
C:Genetics: LIG1
A:Introns: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-372/Product: ligin peroxidase homolog 1 #status predicted <MAT>

Query Match 81.6%; Score 31; DB 2; Length 372;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 199 WMLSAHS 205

RESULT 26
B32322

lignin peroxidase (EC 1.11.1.-) 0282 precursor - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 12-Jul-2004
C:Accession: B32322
R:Schalch, H.; Gaskell, J.; Smith, T.L.; Cullen, D.
Mol. Cell. Biol. 9, 2743-2747, 1989
A:Title: Molecular cloning and sequences of ligin peroxidase genes of Phanerochaete chrysosporium
A:Reference number: A32322; MUID:89343994; PMID:2761543
A:Accession: B32322
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-372 <SCH>
A:Cross-references: UNIPARC:UPI0000175212
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 81.6%; Score 31; DB 2; Length 372;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 199 WMLSAHS 205

RESULT 27
JH0156
lignin peroxidase (EC 1.11.1.-) B precursor - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 12-Jul-2004
C:Accession: JH0156
R:Huponen, K.; Ollikka, P.; Kaelin, M.; Walther, I.; Maentzsaale, P.; Reiser, J.
Gene 89, 145-150, 1990
A:Title: Characterization of ligin peroxidase-encoding genes from ligin-degrading basidiomycetes
A:Reference number: JH0156; MUID:90323600; PMID:2373364
A:Accession: JH0156
A:Molecule type: DNA
A:Residues: 1-372 <HUO>
A:Cross-references: UNIPROT:P31837; UNIPARC:UPI0000168967; GB:M37701; GB:M22720; NID:G161
C:Genetics: lpoB
A:Introns: 21/1; 72/2; 91/2; 163/1; 177/1; 203/2; 344/3; 366/2
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 81.6%; Score 31; DB 2; Length 372;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 199 WMLSAHS 205

RESULT 28
A27817
lignin peroxidase (EC 1.11.1.-) precursor - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 12-Jul-2004
C:Accession: A27817
R:Ritten, M.; Tu, C.P.D.
Nature 326, 520-523, 1987
A:Title: Cloning and sequencing of a cDNA for a liginase from Phanerochaete chrysosporium
A:Reference number: A27817; MUID:87173020; PMID:3561490
A:Accession: A27817
A:Molecule type: mRNA
A:Residues: 1-373 <RIT>
A:Cross-references: UNIPROT:P06181; UNIPARC:UPI0000168965; GB:Y00262; NID:G3149; PIDN:CAV
C:Superfamily: peroxidase
C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-373/Product: ligin peroxidase #status predicted <MAT>

Query Match 81.6%; Score 31; DB 2; Length 373;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|||
Db 199 WMLSAHS 205

RESULT 29
D96955
sensory transduction histidine kinase (HAMP, HsKA, HATPase domains) [imported] - Clostr
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: D96955
R/Noilling, J.; Breton, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: D96955
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-416 <KDR>
A/Cross-references: UNIPROT:Q97LV3; UNIPARC:UPI00000C9E8C; GB:AE001437; PIDN:AAK78431.1;
A/Experimental source: Clostridium acetobutylicum ATCC824
A/Genetics:
A/Gene: CAC0451

Query Match 81.6%; Score 31; DB 2; Length 416;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|||
Db 308 WLEAFS 314

RESULT 30
T48836
hypothetical protein 68B2.200 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C/Accession: T48836
R/Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24541
A/Accession: T48836
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-541 <SCH>
A/Cross-references: UNIPROT:Q9PEV6; UNIPARC:UPI0000069BA5; EMBL:AL353821; GSPDB:GN00112;
A/Experimental source: cosmid contig 68B2, strain 74
C/Genetics:
A/Gene: NCSP:68B2.200
A/Map position: 2
A/Intons: 35/3

Query Match 81.6%; Score 31; DB 2; Length 541;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAF 6
|||
Db 349 WMLSAF 354

RESULT 31
C82120
transcription regulator Arac/XylS family VC2080 [imported] - Vibrio cholerae (strain N16
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: C82120

R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gajim, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82120
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1121 <HEI>
A/Cross-references: UNIPROT:Q9KQC0; UNIPARC:UPI00000C31D3; GB:AE004282; GB:AE003852; NID
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2080
A/Map position: 1

Query Match 81.6%; Score 31; DB 2; Length 1121;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|||
Db 462 WMLSAFS 468

RESULT 32
B53189
cytochrome b560 homolog precursor - Caenorhabditis elegans
N/Alternate names: hypothetical protein T07C4.7
C/Species: Caenorhabditis elegans
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: B53189; S41020
R/Hengartner, M.O.; Horvitz, H.R.
Cell 76, 665-676, 1994
A/Title: Caenorhabditis elegans cell survival gene ced-9 encodes a functional homolog of
A/Reference number: A53189; MUID:94170367; PMID:7907274
A/Accession: B53189
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-182 <HEN>
A/Cross-references: UNIPROT:P41956; UNIPARC:UPI0000126C6F; GB:L26545; NID:9433174; PIDN:
R/Berks, M.
submitted to the EMBL Data Library, January 1994
A/Reference number: S41014
A/Accession: S41020
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-182 <BER>
A/Cross-references: UNIPARC:UPI0000126C6F; EMBL:Z29443; NID:91067051; PID:9443834
C/Genetics:
A/Gene: CYC-1
A/Intons: 29/3; 150/3
C/Superfamily: succinate dehydrogenase cytochrome b560 subunit
C/Keywords: membrane protein; mitochondrion

Query Match 78.9%; Score 30; DB 2; Length 182;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAF 6
|||
Db 67 WMLSGF 72

RESULT 33
T11590
hypothetical protein SPAC17C9.10 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T11590; T52026
R/Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A/Reference number: Z17295

A:Accession: T11590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-271 <BAR>
A:Cross-references: UNIPROT:Q10482; UNIPARC:UPI0000136110; EMBL:Z73099; NID:g1314152
A:Experimental source: strain 972h(-)
R:Kyung Sook, K.S.
submitted to the EMBL Data Library, January 1999
A:Accession: T52026
A:Reference number: 225907
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-271 <KTU>
A:Cross-references: UNIPARC:UPI0000136110; EMBL:L49134; PIDN:AA045180.1
A:Experimental source: strain ED655h(-)
C:Genetics:
A:Map position: IR
A>Note: SPAC17C9.10; stml
C:Superfamily: Saccharomycetes probable membrane protein YBR147w
C:Keywords: transmembrane protein

Query Match 78.9%; Score 30; DB 2; Length 271;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 246 WILGAFS 252

RESULT 34

D96769
hypothetical protein F9B11.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: D96769
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <STD>
A:Cross-references: UNIPROT:Q9CGA2; UNIPARC:UPI00000A6075; GB:AE005173; NID:g10092421; F
C:Genetics:
A:Gene: F9B11.2
A:Map position: 1
C:Superfamily: AAA protein

Query Match 78.9%; Score 30; DB 2; Length 305;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 141 WMLSRYS 147

RESULT 35

G64141
probable tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) HI0059 [similarity] - Haemophilu
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: G64141
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Goeyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: G64141
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-332 <TIGR>
A:Cross-references: UNIPROT:P44491; UNIPARC:UPI00000378C3; GB:U32691; GB:L42023; NID:g15
A>Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: Escherichia coli probable tetraacyldisaccharide 4'-kinase ycaH
C:Keywords: phosphotransferase

Query Match 78.9%; Score 30; DB 2; Length 332;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 12 WMLSPFS 18

RESULT 36

G90322
glycosyltransferase [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90322
R:She, Q.; Singh, R.K.; Cafalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensesen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90322
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <KIR>
A:Cross-references: UNIPROT:Q97XT6; UNIPARC:UPI00000644FE; GB:AE006641; NID:g13814860; PJ
C:Genetics:
A:Gene: SS01619

Query Match 78.9%; Score 30; DB 2; Length 341;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 100 WMLSLFS 106

RESULT 37

B97444
tetraacyldisaccharide 4'-kinase (lipid a 4'-kinase) [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97444
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97444
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <KUR>
A:Cross-references: UNIPROT:Q8UHI5; UNIPARC:UPI000012E91B; GB:AE007869; PIDN:AAK6507.1;
C:Genetics:
A:Gene: AGR_C1257
A:Map position: circular chromosome
C:Superfamily: Escherichia coli probable tetraacyldisaccharide 4'-kinase ycaH

Query Match 78.9%; Score 30; DB 2; Length 348;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 18 WLSLSPFS 24

RESULT 38
AC2662
tetraacyldisaccharide 4'-kinase [imported] - Agrobacterium tumefaciens (strain C58, Dupa
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AC2662
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AC2662
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-348 <KUR>
A/Cross-references: UNIPROT:Q8UH15, UNIPARC:UPI000012E91B; GB:AE008688; PIDN:AAL41713.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Map position: circular chromosome
C/Superfamily: Escherichia coli probable tetraacyldisaccharide 4'-kinase ycaH

Query Match 78.9%; Score 30; DB 2; Length 348;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 18 WLSLSPFS 24

RESULT 39
E82168
probable alpha-1,6-galactosidase VC1690 [imported] - Vibrio cholerae (strain N16961 serc
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: E82168
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: E82168
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-374 <HEI>
A/Cross-references: UNIPROT:Q9KRF2, UNIPARC:UPI00000C3092; GB:AE0044247; GB:AE003852; NID
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:
A/Map position: 1

Query Match 78.9%; Score 30; DB 2; Length 374;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
DB 137 WLSLAF 142

RESULT 40
D82419
tyrosine-specific transport protein VCA0772 [imported] - Vibrio cholerae (strain N16961
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: D82419
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82419
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <HEI>
A/Cross-references: UNIPROT:Q9KLM2, UNIPARC:UPI00000C3641; GB:AE004405; GB:AE003853; NID
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:
A/Map position: 2
C/Superfamily: tyrosine-specific transport protein

Query Match 78.9%; Score 30; DB 2; Length 400;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 45 WMLMAFT 51

RESULT 41
S65138
glycoprotein antigen MGP57/53, mammary gland - bovine (fragment)
N/Alternate names: glycoprotein component 16/major fat-globule membrane protein/MRG-28 h
C/Species: Bos primigenius taurus (cattle)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-Aug-1998
C/Accession: S65138; G48394
R/Aoki, N.; Kishi, M.; Taniguchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 385-391, 1995
A/Title: Molecular cloning of glycoprotein antigens MGP57/53 recognized by monoclonal an
A/Reference number: S65138; MUID:96125736; PMID:8541316
A/Accession: S65138
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-401 <AOK>
A/Cross-references: UNIPARC:UPI0000177B00
R/Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A/Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A/Reference number: A48394; MUID:93250576; PMID:8485470
A/Accession: G48394
A/Status: preliminary
A/Molecule type: protein
A/Residues: 207-220 <MAT>
A/Cross-references: UNIPARC:UPI000014C31B
A/Experimental source: milk
A/Note: sequence extracted from NCBI backbone (NCBI:P.131457)
C/Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homolog
C/Keywords: glycoprotein
F/1-32/Domain: EGF homology (fragment) <EG1>
F/40-79/Domain: EGF homology <EG2>
F/82-239/Domain: discoidin I amino-terminal homology <DNI>
F/243-401/Domain: discoidin I amino-terminal homology <DNI2>

Query Match 78.9%; Score 30; DB 2; Length 401;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
Db 269 WGLSAFS 275

RESULT 42

111743
pP47 protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11743
R:Enslin, M.; Vogel, T.; Calvete, J.J.; Thole, H.H.; Schmitke, J.; Matsuda, T.; Toepfe
Biol. Reprod. 58, 1051-1064, 1998
A:Title: Molecular cloning and characterization of P47, a novel boar sperm-associated zo
A:Reference number: Z17325; MUID:98206817; PMID:9546740
A:Accession: T11743
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-409 <ENS>
A:Cross-references: UNIPROT:P79385; UNIPARC:UPI000012F040; EMBL:Y11683; NID:g2652927; PI
A:Experimental source: testis
C:Function:
A:Description: may be involved in membrane remodeling and/or function as a zona pellucid
A:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homolo
F:6-40/Domain: EGF homology <EGF>

Query Match 78.9%; Score 30; DB 2; Length 409;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
Db 277 WGLSAFS 283

RESULT 43

F95394
probable transmembrane transport protein SMA937 [imported] - Sinorhizobium meliloti (st
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95394
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: F95394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-412 <KUN>
A:Cross-references: UNIPROT:Q92Y26; UNIPARC:UPI00000CB2C5; GB:AEO06469; PIDN:AAK65720.1;
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A86039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA937
A:Genome: plasmid

Query Match 78.9%; Score 30; DB 2; Length 412;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
Db 53 WMLSAFA 59

RESULT 44

AC0546
probable metabolite transport protein STY0387 [imported] - Salmonella enterica subsp. ent
C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0546
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
ch, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-417 <PAR>
A:Cross-references: UNIPARC:UPI000005A472; GB:AL513382; PIDN:CAD008811.1; PID:g16501626; C
A:Genetics:
A:Gene: STY0387

Query Match 78.9%; Score 30; DB 2; Length 417;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAF 6
Db 22 WMLDAF 27

RESULT 45

S74211
PAS-6/7 protein precursor - bovine
N:Alternate names: glycoprotein component 16/major fat-globule membrane protein/MFG-E8 hc
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C:Accession: S74211; S78114; S24181; S65138; G48394
R:Havregard, J.; Andersen, M.H.; Berglund, L.; Rasmussen, J.T.; Petersen, T.E.
Eur. J. Biochem. 240, 628-636, 1996
A:Title: Characterization of glycoprotein PAS-6/7 from membranes of bovine milk fat globu
A:Reference number: S74211; MUID:97008954; PMID:8856064
A:Accession: S74211
A:Molecule type: mRNA
A:Residues: 1-427 <HVA>
A:Cross-references: UNIPROT:Q95114; UNIPARC:UPI000016C359; EMBL:X91895; NID:g1632778; PI
A:Accession: S78114
A:Molecule type: Protein
A:Residues: 19-85; 96-110; 140-165; 174-216; 221-232; 248-277; 285-293; 309-337; 339-420; 425-427
A:Cross-references: UNIPARC:UPI0000177B01; UNIPARC:UPI0000177B02; UNIPARC:UPI0000177B03;
B08; UNIPARC:UPI0000177B09; UNIPARC:UPI0000177B0A
R:Kim, D.H.; Kanno, C.; Mizokami, Y.
Biochim. Biophys. Acta 1122, 203-211, 1992
A:Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from
A:Reference number: S23926; MUID:92353107; PMID:1643094
A:Accession: S24181
A:Molecule type: Protein
A:Residues: 383-394 <KIM>
A:Cross-references: UNIPARC:UPI0000177B08
R:Aoki, N.; Kishi, M.; Taniguchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 385-391, 1995
A:Title: Molecular cloning of glycoprotein antigens MGP57/53 recognized by monoclonal ant
A:Reference number: S65138; MUID:96125736; PMID:8541316
A:Accession: S65138
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 27-427 <AOK>
A:Cross-references: UNIPARC:UPI0000177B00
R:Maicher, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.

A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: G48394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 233-246 <MAT>
A:Cross-references: UNIPARC:UPI000014C318
A:Experimental source: milk
A>Note: sequence extracted from NCBI backbone (NCBIP:131457)
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homolo
C:Keywords: blocked amino end; disulfide bond; glycoprotein; milk
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-427/Product: PAS-6/7 protein #status experimental <MAT>
F:24-58/Domain: EGF homology <EG1>
F:66-105/Domain: EGF homology <EG2>
F:108-265/Domain: discoidin I amino-terminal homology <DN1>
F:269-427/Domain: discoidin I amino-terminal homology <DN2>
F:24-35-29-47-49-58-66-77-71-94-96-105/Disulfide bonds: #status predicted
F:27/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:34/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:59-227/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:109-265-252-256-270-427/Disulfide bonds: #status experimental

Query Match 78.9%; Score 30; DB 2; Length 427;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 295 WGLSAFS 301

RESULT 46
A75444
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75444
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathavan, J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Frazer, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75444
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <WHI>
A:Cross-references: UNIPROT:Q9RVH3; UNIPARC:UPI00000C187D; GB:AE001956; GB:AE000513; NIT
C:Genetic8:
A:Gene: DR1056
A:Map position: 1
C:Superfamily: citrate utilization determinant

Query Match 78.9%; Score 30; DB 2; Length 454;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 54 WMLSAF 59

RESULT 47
F90544
conserved hypothetical protein MYPV_2620 [imported] - Mycoplasma pulmonis (strain UAB CT
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: F90544
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pult
A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: F90544
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <KUR>
A:Cross-references: UNIPROT:Q98Q09; UNIPARC:UPI00000C8046; GB:AL445566; PID:914089675; PJ
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV_2620
C:Superfamily: hypothetical protein MG294

Query Match 78.9%; Score 30; DB 2; Length 467;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 246 WMLSVF 251

RESULT 48
S70171
integral membrane protein - Streptomyces pristinaespiralis
C:Species: Streptomyces pristinaespiralis
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 31-Dec-2004
C:Accession: S70171; S57509
R:Blanc, V.; Salah-Bey, K.; Folcher, M.; Thompson, C.J.
Mol. Microbiol. 17, 989-999, 1995
A:Title: Molecular characterization and transcriptional analysis of a multidrug resistant
A:Reference number: S70171; MUID:96123441; PMID:8596448
A:Accession: S70171
A:Molecule type: DNA
A:Residues: 1-501 <BLA>
A:Cross-references: UNIPROT:Q54806; UNIPARC:UPI00000B6054; EMBL:X84072; NID:9872305; PID
C:Genetics:
A:Gene: ptr

Query Match 78.9%; Score 30; DB 2; Length 501;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 60 WMLNAYS 66

RESULT 49
T40598
hypothetical protein SPBC649.05 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40598
R:Purnelle, B.; Goffeau, A.; Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21939
A:Accession: T40598
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-548 <PUR>
A:Cross-references: UNIPROT:O59755; UNIPARC:UPI0000128686; EMBL:AL023587; PIDN:CAA19047.1
A:Experimental source: strain 972h-; cosmid c649
C:Genetic8:
A:Gene: SPDB:SPBC649.05
A:Map position: 2
A:introns: 3/1

Query Match 78.9%; Score 30; DB 2; Length 548;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 13 WMLKAFS 19

RESULT 50

A39280

glutamate receptor GluR-II precursor - fruit fly (*Drosophila melanogaster*)C;Species: *Drosophila melanogaster*

C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-2004

C;Accession: A39280

R;Schuster, C.M.; Ultsch, A.; Schloess, P.; Cox, J.A.; Schmitt, B.; Betz, H.

Science 254, 112-114, 1991

A;Title: Molecular cloning of an invertebrate glutamate receptor subunit expressed in D.

A;Reference number: A39280; MUID:92022535; PMID:1681587

A;Accession: A39280

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-906 <SCH>

A;Cross-references: UNIPROT:Q24351; UNIPROT:Q9VMP4; UNIPARC:UPI0000177962; GB:M73271

C;Genetics:

A;Gene: FlyBase:Glu-RII

A;Cross-references: FlyBase:FBgn0004620

C;Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor hom

C;Keywords: neurotransmitter receptor

F;431-852/Domain: glutamate receptor homology <GRH>

Query Match

78.9%; Score 30; DB 2; Length 906;

Best local similarity 83.3%; Pred.No. 3e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAF 6

DB 344 WMLGAF 349

Search completed: August 29, 2006, 06:14:15
Job time : 17 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 05:47:27 ; Search time 56 Seconds

(without alignments)
115,627 Million cell updates/sec

Title: US-10-541-343-3

Perfect score: 38

Sequence: 1 WMLSAFS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 500 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	71	2	084G66_CORGL
2	35	92.1	347	2	08N020_HUMAN
3	35	92.1	424	2	05L241_GEOXA
4	35	92.1	459	2	09B6P3_THRSW
5	35	92.1	1760	2	09VLT3_DROME
6	35	92.1	2943	2	034A91_RHOPA
7	34	89.5	147	2	04MR97_BACCE
8	34	89.5	147	2	063CE7_BACCE
9	34	89.5	147	2	06HJV3_BACCH
10	34	89.5	147	2	0813P2_BACCR
11	34	89.5	147	2	0739P8_BACCI
12	34	89.5	147	2	08RPO1_BACCI
13	34	89.5	154	2	03EX04_BACCI
14	34	89.5	211	2	05E524_VIBF1
15	34	89.5	361	2	0744H1_MYCPA
16	34	89.5	458	2	02W9C2_MAGSA
17	34	89.5	637	2	044233_ARTSP
18	34	89.5	843	2	088944_HHRV
19	34	89.5	853	2	03WYR2_PACCN
20	34	89.5	1030	2	073R89_TREDE
21	34	89.5	1196	2	04B833_BURVI
22	34	86.8	44	2	05QTR8_HUMAN
23	33	86.8	304	2	02UD08_ASPPR
24	33	86.8	1404	1	PRG4_HUMAN
25	32	84.2	74	2	046TT1_PALEJ
26	32	84.2	117	2	04S820_TETNG
27	32	84.2	129	2	043Q96_SOLUS
28	32	84.2	159	2	07WXS1_PORGI
29	32	84.2	159	2	07WXS1_PORGI
30	32	84.2	167	2	084S36_ORYSA
31	32	84.2	182	2	04SFB2_TETNG

32	32	84.2	187	1	PUR2_FUGRU	073698 fung rubrip
33	32	84.2	226	2	06CXD3_KULUA	06CXD3 Kuyveromy
34	32	84.2	243	2	06ZRV1_HUMAN	06ZRV1 homo sapien
35	32	84.2	280	2	P72049_MYCTU	P72049 mycobacteri
36	32	84.2	280	2	07TVN9_MYCBO	07TVN9 mycobacteri
37	32	84.2	289	1	MRGRG_MOUSE	091255 mus musculi
38	32	84.2	289	1	0498A2_MOUSE	0498A2 mus musculi
39	32	84.2	333	2	03M9S1_ANAVT	03M9S1 anabena va
40	32	84.2	341	2	02TR7_9DIP	02TR7 dirosophila
41	32	84.2	341	2	02TNS2_9DIP	02TNS2 dirosophila
42	32	84.2	341	2	02TNS6_9DIP	02TNS6 dirosophila
43	32	84.2	341	2	02TNT2_9DIP	02TNT2 dirosophila
44	32	84.2	341	2	02TNT3_9DIP	02TNT3 dirosophila
45	32	84.2	341	2	02TNT5_9DIP	02TNT5 dirosophila
46	32	84.2	341	2	02TNT6_9DIP	02TNT6 dirosophila
47	32	84.2	341	2	02TNT7_DROKX	02TNT7 dirosophila
48	32	84.2	341	2	02TNT9_9DIP	02TNT9 dirosophila
49	32	84.2	341	2	02TNU0_9DIP	02TNU0 dirosophila
50	32	84.2	341	2	02TNU4_9DIP	02TNU4 dirosophila
51	32	84.2	341	2	035CL6_9BRAD	035CL6 bradyrhizob
52	32	84.2	345	2	0820P0_ANASP	0820P0 anabena sp
53	32	84.2	392	2	09KAL1_BACBD	09KAL1 bacillus ha
54	32	84.2	410	2	07WMM4_BORBR	07WMM4 bordetella
55	32	84.2	416	2	07WBE3_BORPA	07WBE3 bordetella
56	32	84.2	452	2	07VUX6_BORPE	07VUX6 bordetella
57	32	84.2	465	1	VP19_EHY1B	P28935 equine herp
58	32	84.2	465	1	VP19_EHY1V	0686P9 equine herp
59	32	84.2	541	2	06Z466_ORYSA	06Z466 oryza sativ
60	32	84.2	551	2	06C2L1_YARLI	06C2L1 yarrowia li
61	32	84.2	564	2	04BH19_BURVI	04BH19 burkholderi
62	32	84.2	569	2	06CB15_YARLI	06CB15 yarrowia li
63	32	84.2	597	2	062DU9_BURMA	062DU9 burkholderi
64	32	84.2	597	2	063UB8_BURPS	063UB8 burkholderi
65	32	84.2	611	2	07WTD1_PACTO	07WTD1 streptomyc
66	32	84.2	740	2	03JXK6_BURPI	03JXK6 burkholderi
67	32	84.2	747	2	06K613_ORYSA	06K613 oryza sativ
68	32	84.2	782	2	06EUL7_ORYSA	06EUL7 oryza sativ
69	32	84.2	872	2	07SE61_NEUCR	07SE61 neurospora
70	32	84.2	876	2	02URH0_ASPPR	02URH0 aspergillus
71	32	84.2	1196	2	03F1S6_9BURK	03F1S6 burkholderi
72	32	84.2	1196	2	044U11_9BURK	044U11 burkholderi
73	32	84.2	1196	2	04LIA7_9BURK	04LIA7 burkholderi
74	32	84.2	1196	2	039KJ6_BURR3	039KJ6 burkholderi
75	32	84.2	1595	2	02USK9_ASPPR	02USK9 aspergillus
76	32	84.2	1595	2	092219_CERSU	092219 cerioporios
77	31	81.6	68	2	092220_CERSU	092220 cerioporios
78	31	81.6	68	2	092267_PAPHY	092267 planenochae
79	31	81.6	70	2	03RUQ2_RALME	03RUQ2 ralsconia m
80	31	81.6	86	2	04AP45_SCHLB	04AP45 chlorobium
81	31	81.6	89	2	03XBG0_METPL	03XBG0 methylobaci
82	31	81.6	99	2	02IE24_9DEL	02IE24 anaeromyxob
83	31	81.6	143	2	09SPH2_GOSHI	09SPH2 gossypium h
84	31	81.6	149	2	09HS18_HALSA	09HS18 halobacteri
85	31	81.6	151	2	071172_IACDI	071172 lactobacilli
86	31	81.6	152	2	05BZT8_SCHUA	05BZT8 schistosoma
87	31	81.6	152	2	06SF57_BACLD	06SF57 bacillus li
88	31	81.6	178	2	06E4A5_CYNDA	06E4A5 cynodon dac
89	31	81.6	178	2	082RP6_STRAW	082RP6 streptomyc
90	31	81.6	249	2	08NKH4_YAGAR	08NKH4 yarrowia li
91	31	81.6	257	2	09KFU2_BACBD	09KFU2 bacillus ha
92	31	81.6	263	2	09K6G9_STRMU	09K6G9 streptococc
93	31	81.6	263	2	087IS4_VIBPA	087IS4 vibrio para
94	31	81.6	210	2	08CVR7_ALTRAT	08CVR7 pseudalter
95	31	81.6	212	2	0425Y0_PLABE	0425Y0 plasmodium
96	31	81.6	249	2	08NKH4_YAGAR	08NKH4 yarrowia li
97	31	81.6	257	2	09KFU2_BACBD	09KFU2 bacillus ha
98	31	81.6	263	2	09K6G9_STRMU	09K6G9 streptococc
99	31	81.6	263	2	087IS4_VIBPA	087IS4 vibrio para
100	31	81.6	274	2	09RCJ3_BACBD	09RCJ3 bacillus ha
101	31	81.6	290	2	08LAS4_ARATH	08LAS4 arabidopsis
102	31	81.6	290	2	04NHS6_WMICC	04NHS6 arabidopsis
103	31	81.6	299	2	08VZ38_ARATH	08VZ38 arabidopsis
104	31	81.6	302	2	07XAM5_ORYSA	07XAM5 oryza sativ

105	31	81.6	317	2	Q5XVF8_ARATH	Q5XVF8_arabidopsis	178	30	78.9	141	2	Q3YK21_CVHNL	Q3YK21_human	coron
106	31	81.6	328	2	Q6ZJ45_BURMA	Q6ZJ45_burkholderi	179	30	78.9	141	2	Q3YK22_CVHNL	Q3YK22_human	coron
107	31	81.6	342	2	Q4FKX6_PELUBA	Q4FKX6_pelagibacte	180	30	78.9	141	2	Q3YK23_CVHNL	Q3YK23_human	coron
108	31	81.6	345	2	Q7LHY5_PHACH	Q7LHY5_phanerochae	181	30	78.9	141	2	Q3YK24_CVHNL	Q3YK24_human	coron
109	31	81.6	347	2	Q43M79_SOLUS	Q43M79_solibacter	182	30	78.9	141	2	Q3YK25_CVHNL	Q3YK25_human	coron
110	31	81.6	347	2	Q4QYG7_98AUR	Q4QYG7_pygopus lep	183	30	78.9	141	2	Q3YK26_CVHNL	Q3YK26_human	coron
111	31	81.6	362	2	Q01785_PHACH	Q01785_phanerochae	184	30	78.9	141	2	Q3YK27_CVHNL	Q3YK27_human	coron
112	31	81.6	365	2	Q8U531_AGR75	Q8U531_agrobacteri	185	30	78.9	141	2	Q3YK28_CVHNL	Q3YK28_human	coron
113	31	81.6	368	2	Q8UC69_AGR75	Q8UC69_agrobacteri	186	30	78.9	141	2	Q3YK29_CVHNL	Q3YK29_human	coron
114	31	81.6	371	1	LIG2_PHACH	P490131 phanerochae	187	30	78.9	141	2	Q3YK30_CVHNL	Q3YK30_human	coron
115	31	81.6	371	1	LIG5_PHACH	P11543 phanerochae	188	30	78.9	141	2	Q3YK31_CVHNL	Q3YK31_human	coron
116	31	81.6	371	2	Q01787_PHACH	Q01787_phanerochae	189	30	78.9	141	2	Q3YK32_CVHNL	Q3YK32_human	coron
117	31	81.6	371	2	Q06326_PHACH	Q06326_phanerochae	190	30	78.9	141	2	Q3YK33_CVHNL	Q3YK33_human	coron
118	31	81.6	372	1	LIG3_PHACH	P21764 phanerochae	191	30	78.9	141	2	Q5XNK6_CVHNL	Q5XNK6_human	coron
119	31	81.6	372	1	LIG6_PHACH	P50622 phanerochae	192	30	78.9	141	2	Q5XNK7_CVHNL	Q5XNK7_human	coron
120	31	81.6	372	1	LIG8_PHACH	P06181 phanerochae	193	30	78.9	141	2	Q5XNK8_CVHNL	Q5XNK8_human	coron
121	31	81.6	372	1	LIGA_PHACH	P31838 phanerochae	194	30	78.9	141	2	Q5XNK9_CVHNL	Q5XNK9_human	coron
122	31	81.6	372	1	LIGB_PHACH	P31838 phanerochae	195	30	78.9	141	2	Q5XNL0_CVHNL	Q5XNL0_human	coron
123	31	81.6	372	2	Q01775_PHACH	Q01775_phanerochae	196	30	78.9	141	2	Q5XNL1_CVHNL	Q5XNL1_human	coron
124	31	81.6	392	2	Q40GS4_9RHOB	Q40GS4_jannaschia	197	30	78.9	141	2	Q5XNL2_CVHNL	Q5XNL2_human	coron
125	31	81.6	406	2	Q63ST5_BURPS	Q63ST5_burkholderi	198	30	78.9	141	2	Q5XNL3_CVHNL	Q5XNL3_human	coron
126	31	81.6	416	2	Q3CG27_THBET	Q3CG27_thermoanaer	199	30	78.9	141	2	Q6B7R4_CVHNL	Q6B7R4_human	coron
127	31	81.6	416	2	Q97LV3_CUOAB	Q97LV3_clostridium	200	30	78.9	141	2	Q6B7R5_CVHNL	Q6B7R5_human	coron
128	31	81.6	421	2	Q5OSM7_ENTHT	Q5OSM7_entamoeba h	201	30	78.9	141	2	Q6B7R6_CVHNL	Q6B7R6_human	coron
129	31	81.6	430	2	Q3JQU4_BURPI	Q3JQU4_burkholderi	202	30	78.9	141	2	Q6B7R7_CVHNL	Q6B7R7_human	coron
130	31	81.6	436	2	Q3P6P2_9GAMM	Q3P6P2_shewanella	203	30	78.9	141	2	Q6B7R8_CVHNL	Q6B7R8_human	coron
131	31	81.6	440	2	Q5LJY0_DROME	Q5LJY0_drosophila	204	30	78.9	141	2	Q6B7R9_CVHNL	Q6B7R9_human	coron
132	31	81.6	441	2	Q7PLM4_DROME	Q7PLM4_drosophila	205	30	78.9	141	2	Q6B7S0_CVHNL	Q6B7S0_human	coron
133	31	81.6	444	2	Q8OPF5_RAJEG	Q8OPF5_raja eglant	206	30	78.9	141	2	Q6B7S1_CVHNL	Q6B7S1_human	coron
134	31	81.6	456	2	Q2RP48_RHORU	Q2RP48_rhodospirill	207	30	78.9	141	2	Q6B7S2_CVHNL	Q6B7S2_human	coron
135	31	81.6	458	2	Q7RL69_PLAYO	Q7RL69_plasmodium	208	30	78.9	141	2	Q6B7S3_CVHNL	Q6B7S3_human	coron
136	31	81.6	472	2	Q8BX72_LACPL	Q8BX72_lactobacill	209	30	78.9	141	2	Q6B7S4_CVHNL	Q6B7S4_human	coron
137	31	81.6	494	2	Q7NNF4_GLOVI	Q7NNF4_gloeobacter	210	30	78.9	141	2	Q6B7S5_CVHNL	Q6B7S5_human	coron
138	31	81.6	494	2	Q4V9P5_BRARE	Q4V9P5_brechydantio	211	30	78.9	141	2	Q6B7S6_CVHNL	Q6B7S6_human	coron
139	31	81.6	541	2	Q9P6V6_TOXCR	Q9P6V6_neurospora	212	30	78.9	149	2	P83695_BREBE	P83695_brevibacill	
140	31	81.6	558	2	Q6BVO5_TOXGO	Q6BVO5_toxoplasma	213	30	78.9	150	2	Q3CTX2_AITAT	Q3CTX2_pseudotaler	
141	31	81.6	640	2	Q5P9M9_AYAMM	Q5P9M9_anaplasmia m	214	30	78.9	155	2	Q6Q1R1_CVHNL	Q6Q1R1_human	coron
142	31	81.6	651	2	Q4S4S0_TETNG	Q4S4S0_tetradon n	215	30	78.9	155	2	Q6Q1R2_CVHNL	Q6Q1R2_human	coron
143	31	81.6	802	2	Q8CEX0_MOUSE	Q8CEX0_mus musculu	216	30	78.9	155	2	Q6Q1R3_CVHNL	Q6Q1R3_human	coron
144	31	81.6	848	2	Q2NFN1_9EURY	Q2NFN1_mechanospha	217	30	78.9	155	2	Q6Q1R4_CVHNL	Q6Q1R4_human	coron
145	31	81.6	999	2	Q4HZU8_GIBZE	Q4HZU8_glibberella	218	30	78.9	155	2	Q6Q1R5_CVHNL	Q6Q1R5_human	coron
146	31	81.6	1121	2	Q9KOCO_VIBCH	Q9KOCO_vibrio chol	219	30	78.9	155	2	Q6Q1R6_CVHNL	Q6Q1R6_human	coron
147	31	81.6	1141	2	Q4QBL6_LEITWA	Q4QBL6_leishmania	220	30	78.9	155	2	Q6Q1R7_CVHNL	Q6Q1R7_human	coron
148	31	81.6	1157	2	Q3WU51_9RHIZ	Q3WU51_mesorhizobi	221	30	78.9	159	2	Q77553_PIG	Q77553_sus scrofa	
149	31	81.6	1183	2	Q5SUQ2_CRYNE	Q5SUQ2_cryptococcu	222	30	78.9	167	2	Q63V54_BURPS	Q63V54_burkholderi	
150	31	81.6	1183	2	Q5KHY2_CRYNE	Q5KHY2_cryptococcu	223	30	78.9	169	2	Q3QCBO_9GAMM	Q3QCBO_shewanella	
151	31	81.6	1464	2	Q4HZM0_GIBZE	Q4HZM0_glibberella	224	30	78.9	169	2	Q637R2_BURPS	Q637R2_burkholderi	
152	31	81.6	1687	2	Q514M1_ENTHT	Q514M1_entamoeba h	225	30	78.9	171	2	Q4HA50_9DEIO	Q4HA50_deinococcus	
153	30	78.9	79	2	Q3S6M6_MARHY	Q3S6M6_marinobacte	226	30	78.9	172	2	Q3BIW0_PBLBD	Q3BIW0_pelotictyon	
154	30	78.9	101	2	Q7UVU0_RHOBA	Q7UVU0_rhodospirill	227	30	78.9	176	2	Q9TV80_PIG	Q9TV80_sus scrofa	
155	30	78.9	112	2	Q4HLM4_CAMLA	Q4HLM4_campylobact	228	30	78.9	177	2	C560_CABEL	C560_caenorhabdi	
156	30	78.9	116	2	Q84UM9_CERHO	Q84UM9_ceratiu ho	229	30	78.9	182	1	Q5VLR7_LEIDO	P41956_leishmania	
157	30	78.9	116	2	Q3OBX5_9H1V1	Q3OBX5_human immun	230	30	78.9	182	1	Q5VLR7_LEIDO	P41956_leishmania	
158	30	78.9	116	2	Q91BN5_9H1V1	Q91BN5_human immun	231	30	78.9	182	1	Q61MM3_LEIMA	Q61MM3_leishmania	
159	30	78.9	116	2	Q2NMQ4_9H1V1	Q2NMQ4_human immun	232	30	78.9	184	1	C560_CABER	C560_caenorhabdi	
160	30	78.9	126	2	Q3P225_9GAMM	Q3P225_shewanella	233	30	78.9	237	2	Q2KMP1_CVHNL	Q2KMP1_human	coron
161	30	78.9	127	2	Q3EUT0_BACTI	Q3EUT0_bacillus th	234	30	78.9	238	2	Q5DIY8_CVHNL	Q5DIY8_human	coron
162	30	78.9	127	2	Q5L227_GEOCKA	Q5L227_geobacillus	235	30	78.9	238	2	Q5DIY9_CVHNL	Q5DIY9_human	coron
163	30	78.9	127	2	Q6RCH1_BACHK	Q6RCH1_bacillus th	236	30	78.9	238	2	Q5DIZ0_CVHNL	Q5DIZ0_human	coron
164	30	78.9	127	2	Q816Q6_BACCR	Q816Q6_bacillus ce	237	30	78.9	238	2	Q5DIZ1_CVHNL	Q5DIZ1_human	coron
165	30	78.9	127	2	Q81KH6_BACAN	Q81KH6_bacillus ac	238	30	78.9	238	2	Q5DIZ3_CVHNL	Q5DIZ3_human	coron
166	30	78.9	131	2	Q3MYI8_9DELT	Q3MYI8_syntrophoba	239	30	78.9	238	2	Q5DIZ4_CVHNL	Q5DIZ4_human	coron
167	30	78.9	138	2	Q3UG79_MOUSE	Q3UG79_mus musculu	240	30	78.9	240	2	Q36JG5_MARHY	Q36JG5_marinobacte	
168	30	78.9	139	2	Q9CZU9_MOUSE	Q9CZU9_mus musculu	241	30	78.9	244	2	Q5X3B1_LEGPA	Q5X3B1_gloeobacter	
169	30	78.9	141	2	Q3OHR3_CVHNL	Q3OHR3_human coron	242	30	78.9	247	2	Q7NIR3_GLOVI	Q7NIR3_gloeobacter	
170	30	78.9	141	2	Q3OHR4_CVHNL	Q3OHR4_human coron	243	30	78.9	251	2	Q211A2_CVHNL	Q211A2_human	coron
171	30	78.9	141	2	Q3OHR5_CVHNL	Q3OHR5_human coron	244	30	78.9	251	2	Q211A3_CVHNL	Q211A3_human	coron
172	30	78.9	141	2	Q3OHR6_CVHNL	Q3OHR6_human coron	245	30	78.9	260	2	Q3UW20_MOUSE	Q3UW20_mus musculu	
173	30	78.9	141	2	Q3OHR7_CVHNL	Q3OHR7_human coron	246	30	78.9	260	2	Q3UW29_MOUSE	Q3UW29_mus musculu	
174	30	78.9	141	2	Q3OHR8_CVHNL	Q3OHR8_human coron	247	30	78.9	262	2	Q81OU1_MOUSE	Q81OU1_mus musculu	
175	30	78.9	141	2	Q3OHR9_CVHNL	Q3OHR9_human coron	248	30	78.9	267	2	Q947B8_ORYSA	Q947B8_oryza sativ	
176	30	78.9	141	2	Q3OHS0_CVHNL	Q3OHS0_human coron	249	30	78.9	271	1	STM1_SCHPO	STM1_schizosacch	
177	30	78.9	141	2	Q3YK20_CVHNL	Q3YK20_human coron	250	30	78.9	271	2	Q5XKZ8_AERHY	Q5XKZ8_aetomonas h	

251	30	78.9	276	2	060M14	CAEBR	060M14	caenorhabdi
252	30	78.9	283	2	051M15	GILPO	051M15	gillibacte
253	30	78.9	288	2	03VB55	SPSPN	03VB55	sphingopyxi
254	30	78.9	298	2	098HR3	RHILIO	098HR3	rhizobium 1
255	30	78.9	302	2	051HB6	BACFN	051HB6	bacteroides
256	30	78.9	302	2	064Y85	BACFR	064Y85	bacteroides
257	30	78.9	305	2	09C6A2	ARATH	09C6A2	arabidopsis
258	30	78.9	313	2	03JTH5	TURPI	03JTH5	turbidopis
259	30	78.9	317	2	07S102	NEUCR	07S102	neurospora
260	30	78.9	318	2	02K576	RHLET	02K576	rhizobium e
261	30	78.9	324	2	08HQJ2	ORNMO	08HQJ2	ornithodoros
262	30	78.9	330	2	07YXL2	TENMO	07YXL2	tenebrio mo
263	30	78.9	332	1	1PXX	HAEIN	1PXX	haemophilus
264	30	78.9	332	2	04OPT5	HAEI8	04OPT5	haemophilus
265	30	78.9	336	1	SYM_BUCAP		SYM_BUCAP	buchnera ap
266	30	78.9	339	2	030YPO	DESDG	030YPO	desulfovibr
267	30	78.9	341	2	097X18	SULSO	097X18	sulfobacill
268	30	78.9	343	2	06ML51	BDEBA	06ML51	bdellovibri
269	30	78.9	346	2	041XP6	METBU	041XP6	methanococc
270	30	78.9	348	1	1PXX	AGRT5	1PXX	agrobacteri
271	30	78.9	355	2	04AEF5	SCHLB	04AEF5	chlorobium
272	30	78.9	374	2	09KRP2	VIBCH	09KRP2	vibrio chol
273	30	78.9	375	2	04B118	9BURK	04B118	polaromonas
274	30	78.9	386	2	05GR5	WOLTR	05GR5	wolbachia s
275	30	78.9	396	2	03S0Z6	RALME	03S0Z6	raistronia m
276	30	78.9	400	2	09K1M2	VIBCH	09K1M2	vibrio chol
277	30	78.9	407	2	03K560	PSEFP	03K560	pseudomonas
278	30	78.9	407	2	049JF5	ECOLI	049JF5	escherichia
279	30	78.9	409	1	MFCGM	PIC	P79385	mus scrofa
280	30	78.9	412	2	092Y26	RHIME	092Y26	rhizobium m
281	30	78.9	413	2	043TL6	SOLUS	043TL6	salmonella
282	30	78.9	417	2	057SK8	SALCH	057SK8	salmonella
283	30	78.9	417	2	05PEX2	SALPA	05PEX2	salmonella
284	30	78.9	417	2	08ZRG4	SALTY	08ZRG4	salmonella
285	30	78.9	417	2	08Z914	SALTY	08Z914	salmonella
286	30	78.9	424	2	04HC05	9DEIO	04HC05	deinococcus
287	30	78.9	427	1	MFCGM	BOVIN	095114	bos taurus
288	30	78.9	431	2	03TOK7	BOVIN	03TOK7	bos taurus
289	30	78.9	443	2	03EFU4	ACTSC	03EFU4	actinobacil
290	30	78.9	445	2	044EVO	CHRSU	044EVO	chromohalob
291	30	78.9	454	2	09RVH3	DEIRA	09RVH3	deinococcus
292	30	78.9	461	2	043MA0	SOLUS	043MA0	solobacter
293	30	78.9	464	2	083X13	STRRO	083X13	streptomyce
294	30	78.9	467	2	098QU9	MYCPU	098QU9	mycoplasma
295	30	78.9	498	2	082FQ8	STRAM	082FQ8	streptomyce
296	30	78.9	501	2	054806	STRPR	054806	streptomyce
297	30	78.9	504	2	06ETI1	ORYSA	06ETI1	oryza sativ
298	30	78.9	504	2	03PS41	NITRHO	03PS41	nitrobacter
299	30	78.9	507	2	09POY3	STRCO	09POY3	streptomyce
300	30	78.9	516	2	03HGA3	TRIER	03HGA3	trichodesmi
301	30	78.9	526	1	TBC19	HUMAN	08H512	homo sapien
302	30	78.9	526	2	09NDX1	HUMAN	09NDX1	homo sapien
303	30	78.9	526	2	08VDV7	MOUSE	08VDV7	mus musculus
304	30	78.9	527	2	05FNM6	XENLA	05FNM6	xenopus lae
305	30	78.9	528	2	075354	ASHGO	075354	aabhyra goss
306	30	78.9	531	2	050UM9	ENTHI	050UM9	entamoeba h
307	30	78.9	533	2	04W9P6	ASPPH	04W9P6	aspergillus
308	30	78.9	537	2	02UNAN3	ASPPR	02UNAN3	aspergillus
309	30	78.9	548	1	CUT12	SCIPO	059755	schizosacch
310	30	78.9	570	2	04H677	9DEIO	04H677	deinococcus
311	30	78.9	605	2	02JUB09	ASPPR	02JUB09	aspergillus
312	30	78.9	606	2	QTVB08	PROMA	QTVB08	prochlorococ
313	30	78.9	616	2	05B8Z5	EMENT	05B8Z5	aspergillus
314	30	78.9	625	2	065DA4	BACLD	065DA4	bacillus 11
315	30	78.9	681	2	09A0B5	9BACN	09A0B5	bacillus sp
316	30	78.9	741	2	038F17	9TRYP	038F17	trypanosoma
317	30	78.9	748	2	07GAL2	ARATH	07GAL2	arabidopsis
318	30	78.9	761	2	09R1V8	ARATH	09R1V8	arabidopsis
319	30	78.9	875	2	04QZV4	LEIMA	04QZV4	leishmania
320	30	78.9	906	2	024351	DROME	024351	drosophila
321	30	78.9	907	2	09VMP4	DROME	09VMP4	drosophila
322	30	78.9	925	2	09ZTAS	ARATH	09ZTAS	arabidopsis
323	30	78.9	974	2	03E4J0	CHILAU	03E4J0	chloroflexu
324	30	78.9	1128	2	060EX7	ORYSA	060EX7	oryza sativ
325	30	78.9	1161	2	048J17	PSEI4	048J17	pseudomonas
326	30	78.9	1190	2	04V0A7	XANCR	04V0A7	xanthomonas
327	30	78.9	1190	2	08PEI3	XANCP	08PEI3	xanthomonas
328	30	78.9	1321	2	04JFH3	CAEBL	04JFH3	caenorhabdi
329	30	78.9	1350	2	061YK0	CAEBR	061YK0	caenorhabdi
330	30	78.9	1372	2	020320	CAEBL	020320	caenorhabdi
331	30	78.9	1525	2	070YF3	GIALA	070YF3	giardia lam
332	30	78.9	1660	2	06C8Z8	YARLI	06C8Z8	varrowia li
333	30	78.9	1809	2	08T398	CTOIN	08T398	ctona intes
334	30	78.9	2140	2	05CVC2	CRYPV	05CVC2	cryptospori
335	30	78.9	2142	2	05CHM9	CRYHO	05CHM9	cryptospori
336	30	78.9	2454	2	07Y1G0	ORYSA	07Y1G0	oryza sativ
337	30	78.9	4055	2	06R1L8	CVHNL	06R1L8	human group
338	30	78.9	6724	2	06R1L8	CVHNL	06R1L8	human group
339	30	78.9	6729	2	06Q1S3	CVHNL	06Q1S3	human coron
340	29	76.3	53	2	08WB30	9NEBP	08WB30	ostreia fu
341	29	76.3	53	2	08WBV9	OSTNU	08WBV9	ostreia fu
342	29	76.3	67	2	03RKTO	RALME	03RKTO	raistronia m
343	29	76.3	80	2	03P271	9GAMM	03P271	shewanella
344	29	76.3	82	2	08VCP7	MOUSE	08VCP7	mus musculu
345	29	76.3	91	2	08M101	STELB	08M101	centrobacter
346	29	76.3	99	2	05DBX2	SCHJA	05DBX2	schistosoma
347	29	76.3	101	2	061G53	DROME	061G53	drosophila
348	29	76.3	105	2	08A5A8	BACFN	08A5A8	bacteroides
349	29	76.3	106	2	03TSW4	MOUSE	03TSW4	mus adult mal
350	29	76.3	114	2	02ZSW3	SHEPU	02ZSW3	shewanella
351	29	76.3	116	2	03Q1Q1	9GAMM	03Q1Q1	shewanella
352	29	76.3	118	2	02X6K2	9GAMM	02X6K2	shewanella
353	29	76.3	123	2	02ZRI0	SHEPU	02ZRI0	xanthomonas
354	29	76.3	119	2	092V24	RHIME	092V24	rhizobium m
355	29	76.3	121	2	02PI177	XANOR	02PI177	xanthomonas
356	29	76.3	123	2	06LYI4	METMP	06LYI4	methanococc
357	29	76.3	133	2	05G169	XANOR	05G169	xanthomonas
358	29	76.3	133	2	0939G4	PSEAC	0939G4	pseudomonas
359	29	76.3	137	2	067N63	SYMTB	067N63	symphobacte
360	29	76.3	138	2	07Q9A1	ANOGA	07Q9A1	anophlebs g
361	29	76.3	139	2	02UDR7	ASPPR	02UDR7	aspergillus
362	29	76.3	141	2	05DCR5	SCHJA	05DCR5	schistosoma
363	29	76.3	142	2	071N46	BACSU	071N46	bacillus su
364	29	76.3	142	2	071N48	BACSU	071N48	bacillus su
365	29	76.3	144	2	071N50	BACSU	071N50	bacillus su
366	29	76.3	146	2	04MFU2	BACCE	04MFU2	bacillus ce
367	29	76.3	146	2	0631P8	BACCE	0631P8	bacillus ce
368	29	76.3	146	2	06HBK8	BACHK	06HBK8	bacillus th
369	29	76.3	146	2	081ZK6	BACCI	081ZK6	bacillus ce
370	29	76.3	146	2	072Y30	BACCI	072Y30	bacillus ce
371	29	76.3	146	2	08RPQ2	BACFN	08RPQ2	bacillus an
372	29	76.3	157	2	05LFPQ9	BACFN	05LFPQ9	bacteroides
373	29	76.3	157	2	09FDN5	BACFR	09FDN5	bacteroides
374	29	76.3	158	2	089YL6	BACTN	089YL6	bacteroides
375	29	76.3	158	2	09KRW6	VIBCH	09KRW6	vibrio chol
376	29	76.3	168	2	046RX2	RALEJ	046RX2	raistronia e
377	29	76.3	171	2	033QRT1	9GAMM	033QRT1	shewanella
378	29	76.3	178	2	065VH4	MANSM	065VH4	mannheimia
379	29	76.3	175	1	DSBB	SHEON	DSBB	shearwater
380	29	76.3	175	2	02ZAF4	9GAMM	02ZAF4	shewanella
381	29	76.3	175	2	035V85	9GAMM	035V85	shewanella
382	29	76.3	178	2	0367U8	9GAMM	0367U8	shewanella
383	29	76.3	186	2	05C112	CRYHO	05C112	cryptospori
384	29	76.3	178	2	03M2Q9	ANAVT	03M2Q9	anabeena va
385	29	76.3	179	1	065VH4	MANSM	065VH4	mannheimia
386	29	76.3	179	1	GMHB	ANETH	GMHB	anethinbac
387	29	76.3	179	2	03Q4E4	9GAMM	03Q4E4	shewanella
388	29	76.3	180	2	03N1A4	9DELTA	03N1A4	syntrichoda
389	29	76.3	186	1	PTH	MYCWS	PTH	mycoplasma
390	29	76.3	201	2	02ST16	MYCCA	02ST16	mycoplasma
391	29	76.3	204	2	08YK77	ANASP	08YK77	anabeena sp
392	29	76.3	205	2	041BC7	KINRA	041BC7	kinococcus
393	29	76.3	207	2	05BVU5	SCHJA	05BVU5	schistosoma
394	29	76.3	218	2	03XA22	METTL	03XA22	metnlobaci
395	29	76.3	219	2	096SP2	HUMAN	096SP2	homo sapien
396	29	76.3	220	1	04E9G8	GRICK	04E9G8	wolbachia e
					Y069	CAREEL		caenorhabdi

397	29	76.3	221	2	Q9VZF3_DROME
398	29	76.3	221	2	Q3K4B4_PSEPP
399	29	76.3	223	2	Q6SR66_BACLD
400	29	76.3	233	2	Q4K3F3_PSEPF
401	29	76.3	234	2	Q7PFU2_AMOGA
402	29	76.3	235	2	Q54S81_DICDI
403	29	76.3	237	2	Q60FR3_PUOY
404	29	76.3	240	2	Q9L3S0_HELPU
405	29	76.3	241	2	Q41HD5_9BACI
406	29	76.3	242	2	Q3W0F8_9ACTO
407	29	76.3	244	2	Q6SD49_BACLD
408	29	76.3	244	2	Q6F8X2_ACTAD
409	29	76.3	244	2	Q6FC28_ACTAD
410	29	76.3	245	2	Q2U9D2_ASPOR
411	29	76.3	249	2	Q4WDG5_ASPFU
412	29	76.3	250	2	Q2KDM6_RHET
413	29	76.3	250	2	Q7RXR2_NEUCR
414	29	76.3	250	2	Q3WPR7_9PHIZ
415	29	76.3	250	2	Q5FIR3_LMACC
416	29	76.3	251	2	Q5RCX0_PONPY
417	29	76.3	252	1	YQGB_BACSU
418	29	76.3	252	1	Q6SHB1_BACLD
419	29	76.3	256	2	Q2T4K1_BURTH
420	29	76.3	256	2	Q5DZ41_VIBF1
421	29	76.3	261	2	Q6S5A7_CABEL
422	29	76.3	268	2	Q2K307_RHET
423	29	76.3	271	2	Q7X916_MALDO
424	29	76.3	273	2	Q7SFX9_LEPIC
425	29	76.3	273	2	Q8EXY9_LEPIC
426	29	76.3	276	2	Q745M4_MYCPA
427	29	76.3	276	2	Q9CDA2_MYCLE
428	29	76.3	278	2	Q21FC7_9DELT
429	29	76.3	279	2	Q25483_HELPU
430	29	76.3	279	2	Q9ZL41_HELPU
431	29	76.3	283	2	Q5GRU6_WOLTR
432	29	76.3	284	2	Q3SD87_9BRAD
433	29	76.3	285	2	Q3BTD7_STRAG
434	29	76.3	290	2	Q59078_ALTYAT
435	29	76.3	290	2	Q6RW45_9GAMM
436	29	76.3	292	2	Q5LIA07_BACFN
437	29	76.3	299	2	Q640B6_BACFR
438	29	76.3	300	2	Q2S7G6_9GAMM
439	29	76.3	300	2	Q3F7E0_9BURK
440	29	76.3	300	2	Q45DK1_9BURK
441	29	76.3	300	2	Q4LWPS_9BURK
442	29	76.3	301	1	REIS_TODPA
443	29	76.3	301	2	Q5RREG3_PONPY
444	29	76.3	301	2	Q8XRN8_PALSO
445	29	76.3	302	1	CTTG_KLEPN
446	29	76.3	302	2	Q73IG4_WOLPM
447	29	76.3	303	2	Q60R86_CABER
448	29	76.3	303	2	Q3QI41_9GAMM
449	29	76.3	303	2	Q51364_PSEAE
450	29	76.3	304	2	Q5DOH1_ECOLI
451	29	76.3	304	2	Q5VCP2_9SAUR
452	29	76.3	305	2	Q5VCP3_9SAUR
453	29	76.3	305	2	Q5VCP4_9SAUR
454	29	76.3	305	2	Q5VCP5_9SAUR
455	29	76.3	305	2	Q5VCP6_9SAUR
456	29	76.3	306	2	Q5LMA1_STIUP
457	29	76.3	310	2	Q31ZK2_RHOPA
458	29	76.3	312	2	Q6F6C2_9ACAR
459	29	76.3	313	2	Q27708_NBPNO
460	29	76.3	315	2	Q871X0_VIBPA
461	29	76.3	319	2	Q2UDV1_ASPOR
462	29	76.3	319	2	Q4HPC0_CAMUP
463	29	76.3	320	2	Q36AF9_9GAMM
464	29	76.3	321	1	CYSP3_HOMAM
465	29	76.3	323	2	Q4SFM9_TETNG
466	29	76.3	325	2	Q48375_BPPI
467	29	76.3	326	2	Q4E7N8_9RICK
468	29	76.3	328	2	Q9T9N2_9RILA
469	29	76.3	331	2	Q5EXH9_MACRS

Q9VZF3	dtrosophila
Q3K4B4	pseudomonas
Q6SR66	bacillus li
Q4K3F3	pseudomonas
Q7PFU2	anopheles g
Q54S81	dictyosteli
Q60FR3	plutella xy
Q9L3S0	helicobacte
Q41HD5	exiguobacte
Q3W0F8	frankia sp.
Q6SD49	bacillus li
Q6F8X2	actinobact
Q6FC28	actinobact
Q2U9D2	aspergillus
Q4WDG5	aspergillus
Q2KDM6	rhizobium e
Q7RXR2	neurospora
Q3WPR7	mesorhizobi
Q5FIR3	lactobacilli
Q5RCX0	pongo pygma
P54485	bacillus su
Q6SHB1	bacillus li
Q2T4K1	burkholderi
Q5DZ41	vibrio fisci
Q6S5A7	caenorhabdi
Q2K307	rhizobium e
Q7X916	malus domes
Q7SFX9	leptospiro
Q8EXY9	leptospiro
Q745M4	mycobacteri
Q9CDA2	mycobacteri
Q21FC7	anaeromyxob
Q25483	helicobacte
Q9ZL41	helicobacte
Q5GRU6	wolbachia s
Q3SD87	bradyrhizob
Q3BTD7	streptococc
Q59078	alteromonas
Q6RW45	psaeromonas
Q5LIA07	bacteroides
Q640B6	bacteroides
Q2S7G6	hahella che
Q3F7E0	burkholderi
Q45DK1	burkholderi
Q4LWPS	burkholderi
P23820	codonarcha p
Q5RREG3	pongo pygma
Q8XRN8	talstonia s
P45414	klebsiella
Q73IG4	wolbachia p
Q60R86	caenorhabdi
Q3QI41	shewanella
Q51364	pseudomonas
Q5DOH1	escherichia
Q5VCP2	rippelleon
Q5VCP3	rippelleon
Q5VCP4	rippelleon
Q5VCP5	rippelleon
Q5VCP6	rippelleon
Q5LMA1	slitobacte
Q31ZK2	rhodospheudo
Q6F6C2	ixodes uria
Q27708	nephrops no
Q871X0	vibrio para
Q2UDV1	aspergillus
Q4HPC0	campylobact
Q36AF9	shewanella
P25784	homatius ame
Q4SFM9	tetrarodon n
Q48375	bacteriopho
Q4E7N8	wolbachia e
Q9T9N2	terebratul
Q5EXH9	macrobrachi

470	29	76.3	335	1	BTUC_PHOLL
471	29	76.3	335	1	IAG2_RAT
472	29	76.3	335	2	Q53G00_HUMAN
473	29	76.3	335	2	Q9H0U3_HUMAN
474	29	76.3	335	2	Q8N8N6_HUMAN
475	29	76.3	335	2	Q5REJ1_PONPY
476	29	76.3	335	2	Q9C0T5_MOUSE
477	29	76.3	335	2	Q9C2T3_MOUSE
478	29	76.3	339	2	Q7B798_PSEAE
479	29	76.3	342	2	Q60ZU2_CABER
480	29	76.3	342	2	Q6BDU8_PERFU
481	29	76.3	342	2	Q2TNR5_9DIPT
482	29	76.3	342	2	Q2TNR6_9DIPT
483	29	76.3	342	2	Q2TNS9_9DIPT
484	29	76.3	346	2	Q649H8_9ARCH
485	29	76.3	347	2	Q9SKJ7_ARATH
486	29	76.3	348	2	Q591V6_MESCR
487	29	76.3	349	2	Q3EGT0_ARATH
488	29	76.3	350	2	Q9SUW2_ARATH
489	29	76.3	351	2	Q9LEF3_ARATH
490	29	76.3	352	1	NUZM_PARLI
491	29	76.3	353	2	Q2S0Z0_9SPHI
492	29	76.3	354	2	Q65X78_ORYSA
493	29	76.3	356	2	Q4EMX4_LISMO
494	29	76.3	356	2	Q8Y4A1_LISMO
495	29	76.3	356	2	Q4S6D4_TETNG
496	29	76.3	361	2	Q8S2P4_ORYSA
497	29	76.3	363	2	Q8FHX9_ECOLI
498	29	76.3	365	2	Q397L4_BURB3
499	29	76.3	367	2	Q4BIV0_BURVI
500	29	76.3	368	2	Q2U1J3_ASPOR

ALIGNMENTS

RESULT 1					
084GE6	CORGL	PRELIMINARY;	PRT;	71 AA.	
AC	084GE6;				
DT	01-JUN-2003,	integrated into UniProtKB/TrEMBL.			
DT	01-JUN-2003,	sequence version 1.			
DT	07-FEB-2006,	entry version 11.			
DE	Hypothetical protein.				
OS	Corynebacterium glutamicum (Brevibacterium flavum).				
OG	Plasmid pCG2.				
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC	Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.				
OX	NCBI_TaxID=1718;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=ATCC 31821.				
RX	MEDLINE=22830013; PubMed=12948627; DOI=10.1016/S0168-1656(03)00157-3;				
RT	Tsuchi A., Puhler A., Kellnowski J., Thierbach G.;				
RT	"Plasmids in Corynebacterium glutamicum and their molecular				
RT	classification by comparative genomics.";				
RT	J. Biotechnol. 104:27-40(2003).				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NoDerivs License				
CC	-----				
DR	EMBL; AY172665; AA018202.1; -; Genomic DNA.				
KW	Hypothetical protein; Plasmid.				
SEQUENCE	71 AA;	7742 MW;	DF8FD8708D007D11	CRC64;	

Query Match 92.1%; Score 35; DB 2; Length 71;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 ||:||||
 Db 58 WMLSAFS 64

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RESULT 2
Q8N0Z0_HUMAN PRELIMINARY; PRT; 347 AA.
ID Q8N0Z0_HUMAN
AC Q8N0Z0;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Seven transmembrane helix receptor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AB065450; BAC05713.1; -; Genomic DNA.
DR EMBL; AB065566; BAC05802.1; -; Genomic DNA.
DR EMBL; AB065486; BAC05739.1; -; Genomic DNA.
DR Ensembl; ENSG00000198822; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like receptor. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgt.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF07562; NCD3G_1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
DR Receptor; Transmembrane.
SQ SEQUENCE 347 AA; 39300 MW; B114CF38477FE624 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 339 WMLSSFS 345

RESULT 3
Q5L241_GEOKA PRELIMINARY; PRT; 424 AA.
ID Q5L241_GEOKA
AC Q5L241;
DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Maltose/maltodextrin transport system (Substrate-binding protein).
DE Oederlouskams-GK0704;
OS Geobacillus kaustophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBI_TaxID=1462;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=HTF426;
RX PubMed=15576355; DOI=10.1093/nar/gkh970;
RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
RA Matsui S., Uchiyama I.;
RT "Thermoadaptation trait revealed by the genome sequence of
RT thermophilic Geobacillus kaustophilus."
RL Nucleic Acids Res. 32:6292-6303(2004).
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DR EMBL; BA000043; BAD74989.1; -; Genomic DNA.
DR GO; GO:0005363; F:maltose transporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0015768; P:maltose transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006060; Maltose_bd.
DR InterPro; IPR006059; SBP_bac_1.
DR InterPro; IPR006061; SBP_dom1.
DR Pfam; PF01547; SBP_bac_1; 1.
DR PRINTS; PR00181; MALTOSEBP.
DR PROSITE; PS01037; SBP_BACTERIAL_1; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 424 AA; 46652 MW; E16D1884B5A5786E CRC64;

Query Match 92.1%; Score 35; DB 2; Length 424;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 310 WMLSAFS 316

RESULT 4
Q9BEF3_THRSW PRELIMINARY; PRT; 459 AA.
ID Q9BEF3_THRSW
AC Q9BEF3;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3) (NADH
DE dehydrogenase subunit 4).
GN Name=NADH4;
OS Thryonomys swinderianus (Greater cane rat).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriocognathi; Thryonomysidae; Thryonomys.
NCBI_TaxID=10169;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21097353; PubMed=11161749; DOI=10.1006/mpev.2000.0870;
RA Mouchaty S.K., Catzeffis F., Janke A., Arnason U.;
RT "Molecular evidence of an African Phiomorpha-South American
RT Mitochondrial genome of the cane rat (Thryonomys swinderianus).";
RL Mol. Phylogenet. Evol. 18:127-135(2001).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 4 family.
CC
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-----
DR EMBL; AJ301644; CAC27808.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport; IEA.
DR InterPro; IPR003918; NADHbd_oxred4.
DR InterPro; IPR010227; NDH_I_M.
DR InterPro; IPR001750; Oxidored_q1.
DR InterPro; IPR000260; Oxidored_q5_N.
DR PANTHER; PTHR11460; NADHbd_oxred4; 1.
DR Pfam; PF00361; Oxidored_q1_1.
DR Pfam; PF01059; Oxidored_q5_N_1.
DR PRINTS; PR01371; NDOXDDBTASB4.
DR TIGRFAMs; TIGR01972; NDH_I_M_1.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 459 AA; 51966 MW; E6DD0150CC0C9F56 CRC64;

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Query Match 92.1%; Score 35; DB 2; Length 459;
 Best Local Similarity 85.7%; Pred. No. 99;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
 Db 359 WMLSSFS 365

RESULT 5
 Q9VLT3_DROME PRELIMINARY; PRT; 1760 AA.
 ID Q9VLT3_DROME
 AC Q9VLT3;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE CG7586-PA (L2D3292P).
 GN Name=Mcr; ORFNames=CG7586, Dmel CG7586;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_taxid=7227;
 OX NCBI [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan P.V., Bouck J., Brokstein P., Brotlier P.,
 RA Buttis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kuip D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537573;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genome perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]

RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskaas R., Smith E.,
 RA Yu C., Rubin G.,
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
 RN [7]

RP STRAIN-Berkeley.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AE003619; AAF52601.1; -; Genomic_DNA.
 CC EMBL; AY058526; AAL13755.1; -; mRNA.
 CC HSSP; P01130; 1A0J.

DR InCase; Q9VLT3; -;
 DR FLYBase; FBgn020240; Mcr.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR011626; A2M comp.
 DR InterPro; IPR002890; A2M_N.
 DR InterPro; IPR011625; A2M_N_2.
 DR InterPro; IPR011627; A2M_rcpt.
 DR InterPro; IPR002172; LDL_rcpt_A.
 DR InterPro; IPR001599; Macroglublna2.

DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF07678; A2M_comp; 1.
 DR Pfam; PF01835; A2M_N; 1.
 DR Pfam; PF07703; A2M_N_2; 1.
 DR Pfam; PF07677; A2M_rcpt; 1.
 DR Pfam; PF00057; ldl_rcpt_a; 1.
 DR SMART; SM00192; LDLa; 1.
 DR PROSITE; PS50068; LDLRA_2; 1.
 DR SEQUENCE 1760 AA; 202783 MW; B8E0602350EB7F86 CRC64;


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Query Match      92.1%; Score 35; DB 2; Length 1760;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
      ||:|||||
Db      966 WMLSAFS 972

RESULT 6
Q34A91_RHOA      PRELIMINARY; PRT; 2943 AA.
AC Q34A91;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Amino acid acetylation.
GN ORFNames=RPCDRAFT_2142;
OS Rhodopseudomonas palustris B12B18.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiales; Rhodopseudomonas.
OX NCBI_TaxID=316056;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B12B18;
RG US DOE Joint Genome Institute (JGI-DOE);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Istrail S., Pittluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Rhodopseudomonas
RT palustris B12B18."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B12B18;
RG US DOE Joint Genome Institute (JGI-DOE);
RA Larimer F., Land M.,
RT "Annotation of the draft genome assembly of Rhodopseudomonas palustris
RT B12B18."
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC
CC EMBL; AALR0100008; EAP1865.1; -; Genomic_DNA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
SQ SEQUENCE 2943 AA; 308266 MW; 358AE8F58262601C CRC64;

Query Match      92.1%; Score 35; DB 2; Length 2943;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
      ||:|||||
Db      1502 WMLSAFS 1508

RESULT 7
Q4MRP7_BACCE      PRELIMINARY; PRT; 147 AA.
AC Q4MRP7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Non-specific DNA-binding protein Dps / iron-binding ferritin-like
DE antioxidant protein / ferroxidase.

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GN Name=dps; ORFNames=BCE_G9241_2031;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RG PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Marden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC
CC EMBL; AAEK0100011; EML14754.1; -; Genomic_DNA.
DR SMR; Q4MRP7; 2-147;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR Interpro; IPR002177; DPS_DNA_bd.
DR Pfam; PF00210; Ferritin_1.
DR PRINTS; PR01346; HELMADAPROT.
DR PRODOM; PD149803; DPS_1.
DR PROSITE; PS00818; DPS_1; 1.
KW DNA-binding.
SQ SEQUENCE 147 AA; 16650 MW; DBA5654D7ED0D77CD CRC64;

Query Match      89.5%; Score 34; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAF 6
      |||||
Db      140 WMLSAF 145

RESULT 8
Q63CE7_BACCC      PRELIMINARY; PRT; 147 AA.
ID Q63CE7;
AC Q63CE7;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Non-specific DNA-binding protein. Dps-like (EC 1.16.3.1).
GN Name=dps; OrderedlocusNames=BCEJ311825;
OS Bacillus cereus (strain ZK / E331).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Chailacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; CP000001; AAU18426.1; -; Genomic_DNA.
DR SMR; Q63CE7; 2-147.

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DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0004322; F:ferroxidase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006950; P:response to stress; IEA.
DR InterPro: IPR002177; DPS_DNA_bd.
DR InterPro: IPR008331; Ferritin_Dps.
DR InterPro: IPR012347; Ferritin_rel.
DR Pfam: PF00210; Ferritin_1.
DR PRINTS: PR01346; HELNAPAPROT.
DR ProDom: PD149803; DPS_1_1.
DR PROSITE: PS00818; DPS_1.
DR Complete proteome; DNA-binding; Oxidoreductase.
SQ SEQUENCE 147 AA; 16707 MW; 2745255C84FCCCCD CRC64;

Query Match      89.5%; Score 34; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 WMLSAF 6
        |||||
Db      140 WMLSAF 145

RESULT 9
06HJV3_BACBK PRELIMINARY; PRT; 147 AA.
ID 06HJV3_BACBK
AC 06HJV3
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Non-specific DNA-binding protein Dps (EC 1.16.3.1).
GN Name=dps; OrderedLocNames=BT9727.1841;
OS Bacillus thuringiensis subsp. konkukian;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=97-27;
RC Bietlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27."
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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DR EMBL: AE017355; AAT63428.1; -; Genomic_DNA.
DR SMR: 06HJV3; 2-147.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0004322; F:ferroxidase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006950; P:response to stress; IEA.
DR InterPro: IPR002177; DPS_DNA_bd.
DR InterPro: IPR008331; Ferritin_Dps.
DR InterPro: IPR012347; Ferritin_rel.
DR Pfam: PF00210; Ferritin_1.
DR PRINTS: PR01346; HELNAPAPROT.
DR ProDom: PD149803; DPS_1_1.
DR PROSITE: PS00818; DPS_1.
DR Complete proteome; DNA-binding; Oxidoreductase.
SQ SEQUENCE 147 AA; 16707 MW; 2745255C84FCCCCD CRC64;

Query Match      89.5%; Score 34; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 WMLSAF 6
        |||||
Db      140 WMLSAF 145

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Db      140 WMLSAF 145
        |||||

RESULT 10
0813P2_BACCR PRELIMINARY; PRT; 147 AA.
ID 0813P2_BACCR
AC 0813P2
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Non-specific DNA-binding protein Dps / Iron-binding ferritin-like
DE antioxidant protein / Ferroxidase (EC 1.16.3.1).
GN OrderedLocNames=BC2011; ORFNames=BC_2011.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RX Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kaparatel V., Bhatnagar A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Malinas T.,
RA Grechkin Y., Fusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyriakides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
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-----
DR EMBL: AE016877; AAP08980.1; -; Genomic_DNA.
DR HSSP: Q8RP01; 141G.
DR SMR: 0813P2; 2-147.
DR BiOCyc: BCR226900.BC2011-MONOMER; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0004322; F:ferroxidase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006950; P:response to stress; IEA.
DR InterPro: IPR002177; DPS_DNA_bd.
DR InterPro: IPR008331; Ferritin_Dps.
DR InterPro: IPR012347; Ferritin_rel.
DR Pfam: PF00210; Ferritin_1.
DR PRINTS: PR01346; HELNAPAPROT.
DR ProDom: PD149803; DPS_1_1.
DR PROSITE: PS00818; DPS_1.
DR Complete proteome; DNA-binding; Oxidoreductase.
SQ SEQUENCE 147 AA; 16680 MW; 36A4D54D650CCCCD CRC64;

Query Match      89.5%; Score 34; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 WMLSAF 6
        |||||
Db      140 WMLSAF 145

RESULT 11
0739P8_BACCI PRELIMINARY; PRT; 147 AA.
ID 0739P8_BACCI
AC 0739P8
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 14.
DE General stress protein.
GN Name=dps; ORFNames=BCE_2092;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

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OC Bacillus cereus group.
OX NCBI_TaxID=222523;

[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=1960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiloul S.V., Kolonay J.F.,
RA Nelson W.C., Kolsto A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).

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EMBL; AE017194; AAS41013.1; -; Genomic_DNA.
DR SMR; Q739P8; 2-147.
DR GenomeReviews; AE017194 GR; dps.
DR GO; GO:0008199; F: ferric iron binding; IEA.
DR GO; GO:0006950; P: response to stress; IEA.
DR GO; GO:0006950; P: response to stress; IEA.
DR InterPro; IPR02177; DPS_DNA_bd.
DR InterPro; IPR008331; Ferritin_Dps.
DR Pfam; PF00210; Ferritin; 1.
DR PRINTS; PR01346; HEINAPAPROT.
DR ProDom; PD149803; DPS_1.
DR PROSITE; PS00818; DPS_1; 1.
KM Complete proteome.
SQ SEQUENCE 147 AA; 16707 MW; 2745255C84FCCCD CRC64;

Query Match 89.5%; Score 34; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 140 WMLSAF 145

RESULT 12
08RP01 BACAN PRELIMINARY; PRT; 147 AA.
AC 08RP01; Q6HZV3; Q6KTT5; Q81RM9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-MAR-2006, entry version 25.
DE Miniferritin Dlp2 (General stress protein).
GN Name=dlp2; Synonyms=dps; OrderedLocustNames=BA2013, BAS1871, GBA2013;
GN ORNames=BA_2013;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;

[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21964043; PubMed=11836250; DOI=10.1074/jbc.M112378200;
RA Papiunuto E., Dundon W.G., Pitulis N., Battistutta R., Montecucco C.,
RA Zanotti G.;
RT "Structure of two iron-binding proteins from Bacillus anthracis.";
RL J. Biol. Chem. 277:15093-15098(2002).

[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RT 07-FEB-2006, entry version 1.
DE Non-specific DNA-binding protein Dps / Iron-binding ferritin-like
DE antioxidant protein / Peroxidase (EC 1.16.3.1).
GN ORNames=BMT 06140;
OS Bacillus thuringiensis serovar israelensis ATCC 35646.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=339854;
RN Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niernan W.C.,

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RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolsto A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).

[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames ancestor;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Stearie;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Stearne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

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EMBL; AF374269; AAM18636.1; -; Genomic_DNA.
DR EMBL; AE016879; AAP25903.1; -; Genomic_DNA.
DR EMBL; AE017225; AAT54186.1; -; Genomic_DNA.
DR EMBL; AE017343; AAT31135.1; -; Genomic_DNA.
DR PDB; 1JIG; X-ray; A/B/C/D-2-147.
DR GenomeReviews; AE016879 GR; BA2013.
DR GenomeReviews; AE017225 GR; BAS1871.
DR GenomeReviews; AE017334 GR; GBA2013.
DR TIGR; BA2013; -.
DR TIGR; GBA2013; -.
DR GO; GO:0008199; F: ferric iron binding; IEA.
DR GO; GO:0006950; P: iron ion homeostasis; IEA.
DR GO; GO:0006950; P: response to stress; IEA.
DR GO; GO:0006950; P: response to stress; IEA.
DR InterPro; IPR02177; DPS_DNA_bd.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR01347; Ferritin_rel.
DR Pfam; PF00210; Ferritin; 1.
DR PRINTS; PR01346; HEINAPAPROT.
DR ProDom; PD149803; DPS_1.
DR PROSITE; PS00818; DPS_1; 1.
KM Complete proteome.
SQ SEQUENCE 147 AA; 16649 MW; 2741651884FCCCD CRC64;

Query Match 89.5%; Score 34; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
Db 140 WMLSAF 145

RESULT 13
03EX04 BACTI PRELIMINARY; PRT; 154 AA.
ID 03EX04_BACTI
AC 03EX04;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Non-specific DNA-binding protein Dps / Iron-binding ferritin-like
DE antioxidant protein / Peroxidase (EC 1.16.3.1).
GN ORNames=BMT 06140;
OS Bacillus thuringiensis serovar israelensis ATCC 35646.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=339854;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35646;
 RA Anderson I., Sorokin A., Kapral V., Reznik G., Bhattacharya A.,
 RA Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
 RA D'Souza M., Larsen N., Pusch G., Liolios K., Greekin Y., Lipidus A.,
 RA Goldsman E., Chu L., Feinstein M., Ehrlich D., Overbeek R.,
 RA Kyrpides N., Ivanova N.;
 RT "Comparative genome analysis of *Bacillus cereus* group genomes with
 RT *Bacillus subtilis*.";
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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DR EMBL; AAJ01000037; EA056104.1; -; Genomic_DNA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008199; F:ferri iron binding; IEA.
 DR GO; GO:0004322; F:ferroxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006950; P:response to stress; IEA.
 DR InterPro; IPR002177; DBS_DNA_Bd.
 DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR012347; Ferritin_rel.
 DR Pfam; PF00210; Ferritin_1.
 DR PRINTS; PR01346; HELNAPAPROT.
 DR PRODOM; PD149803; DPS; 1.
 DR PROSITE; PS00818; DPS_1.1.
 DR DNA-binding; Oxidoreductase.
 SQ SEQUENCE 154 AA; 17397 MW; 1C179A213C87D3C0 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAF 6
 |||||
 Db 147 WMLSAF 152

RESULT 14
 Q5E524 VIBF1 PRELIMINARY; PRT; 211 AA.
 AC Q5E524;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Lysine exporter protein.
 GN OrderedLocustNames=VF1057;
 OS *Vibrio fischeri* (strain ATCC 700601 / ES114).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC Vibrionaceae; Vibrrio.
 CC NCBI_TaxID=312309;
 CC [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15703294; DOI=10.1073/pnas.0409900102;
 RA Ruby E.G., Urbanowski M., Campbell U., Dunn A., Faini M., Gonsalus R.,
 RA Loshron P., Lupp C., McCam J., Millikan D., Schaefer A., Stabb E.,
 RA Stevens A., Vaisick K., Whistler C., Greenberg E.P.;
 RT "Complete genome sequence of *Vibrio fischeri*: a symbiotic bacterium
 RT with pathogenic congeners.";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
 CC -----
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DR EMBL; CP0000020; AAM8552.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005293; F:lysine permease activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.

DR InterPro; IPR001123; Lyse.
 DR Pfam; PF01810; Lyse; 1.
 KW Complete proteome.
 SQ SEQUENCE 211 AA; 22582 MW; F69806C1F7B1D5D9 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAF 6
 |||||
 Db 203 WMLSAF 208

RESULT 15
 Q744H1 MYCPA PRELIMINARY; PRT; 361 AA.
 ID Q744H1 MYCPA
 AC Q744H1;
 DT 05-JUN-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUN-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Hypothetical protein.
 GN OrderedLocustNames=MAP0370; ORFNames=MAP_0370;
 OS *Mycobacterium paratuberculosis*.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 CC *Mycobacterium avium* complex (MAC).
 CC NCBI_TaxID=1770;
 CC [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=X10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -----
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DR EMBL; AE016958; AAS02687.1; -; Genomic_DNA.
 DR InterPro; IPR005614; NtFD.
 DR Pfam; PF03916; NtFD; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 361 AA; 37516 MW; 9AACB052006E772C CRC64;

Query Match 89.5%; Score 34; DB 2; Length 361;
 Best Local Similarity 85.7%; Pred. No. 1,36+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
 |||||
 Db 138 WMLSAFS 144

RESULT 16
 Q2W9C2 MAGSA PRELIMINARY; PRT; 458 AA.
 ID Q2W9C2 MAGSA
 AC Q2W9C2;
 DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 10-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 4.
 DE Permease of the major facilitator superfamily.
 GN ORFNames=amb0749;
 OS *Magnetospirillum magneticum* AMB-1.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 CC Rhodospirillaceae; Magnetospirillum.
 CC NCBI_TaxID=342108;
 CC [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AMB-1;
 RX PubMed=16303747;
 RA Matsunaga T., Okamura Y., Fukuda Y., Mahyudi A.T., Murase Y.,
 RA Takeyama H.;
 RT "Complete Genome Sequence of the Facultative Anaerobic Magnetotactic
 RT Bacterium *Magnetospirillum* sp. strain AMB-1.";

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RL  DNA Res. 12:157-166(2005).
CC  -1- SUBCELLULAR LOCATION: Inner membrane; multi-pass membrane protein
CC  (by similarity).
CC  -----
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CC  -----
DR  EMBL: AP007255; BAB9553.1; -; Genomic DNA.
KW  Inner membrane; Membrane; Transmembrane; Transport.
SQ  SEQUENCE 458 AA; 48181 MW; 6F13CC647D77468B CRC64;

Query March 89.5%; Score 34; DB 2; Length 458;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 WMLSAFS 7
    |||||
Db  226 WILSAFS 232

RESULT 17
Q44233 ARTSP PRELIMINARY; PRT; 637 AA.
ID  Q44233 ARTSP PRELIMINARY; PRT; 637 AA.
AC  Q44233;
DT  01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT  01-NOV-1996, sequence version 1.
DT  07-FEB-2006, entry version 20.
DE  Beta-galactosidase.
OS  Arthrobacter sp.
OC  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC  Micrococciaceae; Micrococcaceae; Arthrobacter.
OX  NCBI_TaxId=1667;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=95238267; PubMed=7721689;
RA  Guthrie L.R., Trimbur D.E., Kasmlir J.E.;
RT  "Analysis of a novel gene and beta-galactosidase isozyme from a
RT  psychrotrophic Arthrobacter isolate.";
RL  J. Bacteriol. 177:1981-1988(1995).
CC  -----
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CC  -----
DR  EMBL: U17417; AAA75601.1; -; Genomic DNA.
DR  GO: GO:0009341; C:beta-galactosidase complex; IEA.
DR  GO: GO:0004565; F:beta-galactosidase activity; IEA.
DR  GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR  InterPro: IPR003476; Glyco_hydro_42.
DR  Pfam: PF02448; Glyco_hydro_42; 1.
DR  PIRSF: PIRSF001084; B-galactosidase; 1.
SQ  SEQUENCE 637 AA; 70895 MW; 9816DB4FCC3A728C CRC64;

Query March 89.5%; Score 34; DB 2; Length 637;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 WMLSAFS 7
    |||||
Db  372 WMLSCFS 378

RESULT 18
P88944 HHV8 PRELIMINARY; PRT; 843 AA.
ID  P88944 HHV8 PRELIMINARY; PRT; 843 AA.
AC  P88944;
DT  01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT  01-MAY-1997, sequence version 1.
DT  07-FEB-2006, entry version 23.
DE  ORF 56 (DNA replication protein).
OS  Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC  Viruses; dAdna viruses 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC  Gammaherpesvirinae; Rhadinovirus.
OX  NCBI_TaxId=37296;

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RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;
RA  Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT  "Molecular mimicry of human cytokine and cytokine response pathway
RT  genes by KSHV.";
RL  Science 274:1739-1744(1996).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
RA  Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA  Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT  "Nucleotide sequence of the Kaposi's sarcoma-associated herpesvirus
RT  (HHV8)";
RL  Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RA  Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA  Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL  Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN  [4]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=97296220; PubMed=9151804;
RA  Neipel F., Albrecht J.-C., Fleckenstein B.;
RT  "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT  human herpesvirus 8: determinants of its pathogenicity?";
RL  J. Virol. 71:4187-4192(1997).
RN  [5]
RP  NUCLEOTIDE SEQUENCE.
RA  Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA  Friedmann-Kien A.E., Fleckenstein B.;
RT  "The genome of human herpesvirus 8 cloned from Kaposi's sarcoma.";
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC  -----
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CC  -----
DR  EMBL: U75698; AAC57138.1; -; Genomic DNA.
DR  EMBL: U93872; AAB62614.1; -; Genomic DNA.
DR  GO: GO:0003896; F:DNA primase activity; IEA.
DR  GO: GO:0006260; P:DNA replication; IEA.
DR  InterPro: IPR004340; UL52 UL70.
DR  Pfam: PF03121; Herpes UL52; 1.
SQ  SEQUENCE 843 AA; 95554 MW; 89248BFCB7DBAB0E CRC64;

Query March 89.5%; Score 34; DB 2; Length 843;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 WMLSAF 6
    |||||
Db  161 WMLSAF 166

RESULT 19
Q3WYR2 9ACTN PRELIMINARY; PRT; 853 AA.
ID  Q3WYR2 9ACTN PRELIMINARY; PRT; 853 AA.
AC  Q3WYR2;
DT  11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT  11-OCT-2005, sequence version 1.
DT  07-MAR-2006, entry version 6.
DE  Valyl-tRNA synthetase, class 1a.
OS  ORFNames=Exy1DRAFT_0191;
OC  Bacteria; Actinobacteria; Rubrobacteridae; Rubrobacterales;
OC  Rubrobacteriaceae; Rubrobacteraceae; Rubrobacter.
OX  NCBI_TaxId=266117;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  STRAIN=DSM 9941;
RG  US DOE Joint Genome Institute (JGI-PGF);
RA  Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA  Hammon N., Ierani S., Pitluck S., Richardson P.;

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RT "Sequencing of the draft genome and assembly of Rubrobacter
RT xylanophilus DSM 9941."
RL Submitted (JUL-2005) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-DSM 9941;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Rubrobacter xylanophilus
RT DSM 9941."
RL Submitted (JUL-2005) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-DSM 9941;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ierant S., Pritchuck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
CC EMBL: AAE0200094; FAN4753.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016874; F:Ligase activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004832; F:valine-tRNA ligase activity; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0006438; P:valyl-tRNA aminoacylation; IEA.
DR InterPro: IPR002300; tRNA-synt_1a.
DR InterPro: IPR001412; tRNA-synt_1.
DR InterPro: IPR002303; tRNA-synt_val.
DR Pfam: PF00133; tRNA-synt_1; 1.
DR PRINTS: PR00986; TRNASYNTHAL.
DR TIGRfams: TIGR00422; vals; 1.
DR PROSITE: PS00178; AA_TRNA_LIGASE_1; 1.
DR ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding;
DR protein biosynthesis.
SQ SEQUENCE 853 AA; 97415 MW; 6E63E5A9C56B32D CRC64;

Query Match 89.5%; Score 34; DB 2; Length 853;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
DB 607 WILSAFS 613

RESULT 20
O73RB9 TREDE PRELIMINARY; PRT: 1030 AA.
AC O73RB9_
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 20.
DE Nuclease ShcCD, C subunit, putative.
GN OrderedLocustNames=TDE0171; ORFNames=TDE_0171;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 35405 / DSM 14222;
RC PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelein H., Eisen J.A., Heidelberg J.F.,

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RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajd D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.U., Frazer C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes."
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
CC -----
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CC -----
CC EMBL: AE017226; AAS10668.1; -; Genomic_DNA.
DR TIGR: TDE0171; -;
DR GenomeReviews: AE017226_GR; TDE0171.
DR BioCyc: TDE0171; TDE0171-MONOMER; -;
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016887; F:ATPase activity; IEA.
DR InterPro: IPR003439; ABC_transp_like.
DR Complete proteome.
SQ SEQUENCE 1030 AA; 117667 MW; EA7480ED35817387 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 1030;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAF 6
DB 877 WMLSAF 882

RESULT 21
O4B833 BURVI PRELIMINARY; PRT: 1196 AA.
ID O4B833_
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Pyruvate decarboxylase; Pyruvate ferredoxin/flavodoxin oxidoreductase.
GN ORFNames=Bcep1808DRPT_0224;
OS Burkholderia vietnamiensis G4.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269482;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ierant S., Pritchuck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4."
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia vietnamiensis
RT G4."
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ierant S., Pritchuck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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CC -----
DR EMBL: AAEH0200080; EAM26009.1; -; Genomic DNA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
KW Purvate.
SQ SEQUENCE 1196 AA; 129821 MW; 69FF40127361D3F4 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 1196;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAF 6
DB 1091 WMLSAF 1096

RESULT 22
Q5QTR8_HUMAN PRELIMINARY; PRT; 44 AA.
AC Q5QTR8;
DT 04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DT 07-FEB-2006, entry version 4.
DS Putative P008-2.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RA Liu B., Zhao B., Zhang X.Y., Xu Y.Y., Liu Y.Q., Song L., Ye J.,
RA Sheng H., Gao Y., Wang X.L., Wei Y.J., Zhang J., Song L., Jiang Y.X.,
RA Zhao Z.W., Ding J.F., Liu L.S., Gao R.L., Wu Q.Y., Qiang B.O.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.,
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AF109190; AAQ13500.1; -; mRNA.
SQ SEQUENCE 44 AA; 5210 MW; 90754272D3B001A4 CRC64;

Query Match 86.8%; Score 33; DB 2; Length 44;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 9 WMLSAFS 15

RESULT 23
Q2UD08_ASPOR PRELIMINARY; PRT; 304 AA.
AC Q2UD08;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 1.
DT 07-MAR-2006, entry version 3.
DR HydroLase of the alpha/beta superfamily.
GN ORFNames=AO090012000367;
OS Aspergillus oryzae.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIB 40;
RC PubMed=16372010; DOI=10.1038/nature04300;
RX

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RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terao G.,
RA Kusumoto K., Arita T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA Horikuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Hagiwara J.E., Nieman W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhattacharya D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Isono K.,
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA Kuhnara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae.";
RL Nature 438:1157-1161(2005).
CC -----
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CC -----
DR EMBL: AP007161; BAB60557.1; -; Genomic DNA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
KW HydroLase.
SQ SEQUENCE 304 AA; 33626 MW; A3D3EA35882B9D6A CRC64;

Query Match 86.8%; Score 33; DB 2; Length 304;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 168 WMLSLFS 174

RESULT 24
PRG4_HUMAN STANDARD; PRT; 1404 AA.
ID PRG4_HUMAN
AC Q92954; O6DNC4; O6DNC5; O6ZM25; Q9BX49;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2005, entry version 2.
DT 07-MAR-2006, entry version 38.
DE Proteoglycan-4 precursor (ubridicin) (megakaryocyte stimulating factor)
DE (Superficial zone proteoglycan) [Contains: Proteoglycan-4 C-terminal
DE part].
GN Name=PRG4; Synonyms=MSP, SZP;
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM A), AND VARIANT TRP-180.
RA Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C.,
RA Kelleher K., Giannotti J., Calvetti J., Fitzgerald M., Kriz M.J.,
RA Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Geisner T.,
RA Bhatia S., Kriz R., Hewick R., Clark S.C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM E).
RC TISSUE=Synovial cell;
RC PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Odayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,
RA Yamakami K., Yaeuda T., Iwayanagi T., Wagatsuma Y., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano Y.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mutsaers K., Yuuki H., Oshima A., Sasaki N., Aotaka S.,

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RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Komiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Matanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Matanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Oimoto Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Oktani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Matanabe M., Komatsu T.,
 RA Minushima-Sugano J., Satoh T., Shirai Y., Takahashi T., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita K.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RL [3]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RP Human chromosome 1 international sequencing consortium;
 RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 32-193 AND 1148-1398.
 RP Jones A.R., Hughes C.E., Flannery C.R., Caterson B.,
 RA "Cloning and production of recombinant PRG4/cartilage superficial zone
 RT proteoglycan (SZP) N- and C-terminal domains.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 39-90; 158-258 AND 1209-1295, AND
 RP IDENTIFICATION OF ISOFORM C.
 RX MEDLINE=99120896; PubMed=9920774; DOI=10.1006/dbrc.1998.0104.
 RA Flannery C.R., Hughes C.E., Schumacher B.L., Tudor D., Aydelotte M.B.,
 RA Kuettner K.E., Caterson B.,
 RT "Articular cartilage superficial zone protein (SZP) is homologous to
 RT megakaryocyte stimulating factor precursor and is a multifunctional
 RT proteoglycan with potential growth-promoting, cytoprotective, and
 RT lubricating properties in cartilage metabolism.";
 RL Biochem. Biophys. Res. Commun. 254:535-541(1999).
 RL [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 41-376 (ISOFORM F), FUNCTION, AND
 RP SUBCELLULAR LOCATION.
 RC Tissue=Fetal liver;
 RX PubMed=14976050; DOI=10.1182/blood-2003-06-1825.
 RA Liu Y.-J., Lu S.H., Xu B., Yang R.C., Ren Q., Liu B., Li B., Lu M.,
 RA Yan F.Y., Han Z.B., Han Z.C.,
 RT "Hemangiopoietin, a novel human growth factor for the primitive cells
 RT of both hematopoietic and endothelial cell lineages.";
 RL Blood 103:4449-4456(2004).
 RL [7]
 RP PURIFICATION.
 RP Tissue=Urine;
 RA Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C.,
 RA Kuettner K., Giannotti J., Calvetti J., Fitzgerald M., Kriz M.-J.,
 RA Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesser T.,
 RA Bhargava S., Kriz R., Hewick R., Clark S.C.,
 RT "Purification, biochemical characterization, and cloning of a novel
 RT megakaryocyte stimulating factor that has megakaryocyte colony
 RT stimulating activity.";
 RL Blood 78:279A-279A(1991).
 RL [8]
 RP GENE STRUCTURE.
 RA Metberg D.M., Fitz L.J., Temple P., Giannotti J., Murtha P.,
 RA Fitzgerald M., Scaltrito H., Kuettner K., Preissner K., Kriz R.,
 RA Jacobs K., Turner K.,
 RT "A comparison of vitronectin and megakaryocyte stimulating factor.";
 RL (In) Preissner K.T., Rosenblatt S., Kost C., Wegerhoff J.,
 MOsher D.F. (eds.),
 RL Biology of vitronectins and their receptors, pp.45-52, Elsevier
 RL Science Publishers B.V., Amsterdam (1993).
 RL [9]
 RP GLYCOSYLATION.
 RX MEDLINE=94241694; PubMed=8185311; DOI=10.1006/abbi.1994.1219;
 RA Schumacher B.L., Block J.A., Schmid T.M., Aydelotte M.B.,

RA Kuettner K.E.;
 RT "A novel proteoglycan synthesized and secreted by chondrocytes of the
 RT superficial zone of articular cartilage.";
 RL Arch. Biochem. Biophys. 311:144-152(1994).
 RL [10]
 RP TISSUE SPECIFICITY, AND INVOLVEMENT IN CACP.
 RX PubMed=10545950; DOI=10.1038/154496;
 RA Marcelino J., Carpen O.D., Suwaite W.M., Gutierrez O.M., Schwartz S.,
 RA Robbins C., Sood R., Makalowska I., Baxevanis A., Johnstone B.,
 RA Laxer R.M., Zemel L., Kim C.A., Herd J.K., Ihle J., Williams C.,
 RA Johnson M., Ramon V., Alonso L.G., Brunoni D., Gerstein A.,
 RA Papadopoulos N., Bahabri S.A., Trent J.M., Warman M.L.,
 RT "CACP, encoding a secreted proteoglycan, is mutated in campodactyl-
 RT arthropathy-coxa vara-pericarditis syndrome.";
 RL Nat. Genet. 23:319-322(1999).
 RL [11]
 RP TISSUE SPECIFICITY, AND IDENTIFICATION OF ISOFORMS B; C AND D.
 RX MEDLINE=20573856; PubMed=11124536;
 RA Ikegawa S., Sano M., Koshizuka Y., Nakamura Y.,
 RT "Isolation, characterization and mapping of the mouse and human PRG4
 RT (proteoglycan 4) genes.";
 RL Cytogenet. Cell Genet. 90:291-297(2000).
 RL [12]
 RP IDENTIFICATION BY MASS SPECTROMETRY, FUNCTION, AND GLYCOSYLATION.
 RX PubMed=10743795;
 RA Day G.D., Britz D.E., Cha C.-J.,
 RT "Lubricin is a product of megakaryocyte stimulating factor gene
 RT expression by human synovial fibroblasts.";
 RL J. Rheumatol. 27:594-600(2000).
 RL [13]
 RP CARBOHYDRATE-LINKAGE SITE ASN-1159.
 RX PubMed=16335952; DOI=10.1021/pr0502065;
 RA Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
 RA Moore R.J., Smith R.D.,
 RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
 RT hydrazone chemistry, and mass spectrometry.";
 RL J. Proteome Res. 4:2070-2080(2005).
 RL [14]
 RP FUNCTION: Plays a role for boundary lubrication within
 CC articulating joints. Prevents protein deposition onto cartilage
 CC from synovial fluid, control adhesion-dependent synovial growth,
 CC and inhibit the adhesion of synovial cells to the cartilage
 CC surface.
 CC -!- FUNCTION: Isoform F play a role as a growth factor acting on the
 CC primitive cells of both hematopoietic and endothelial cell
 CC lineages.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=A;
 CC IsoId=Q92954-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=Q92954-2; Sequence=VSP_016467;
 CC Name=C;
 CC IsoId=Q92954-3; Sequence=VSP_016468;
 CC Name=D;
 CC IsoId=Q92954-4; Sequence=VSP_016467, VSP_016468;
 CC Name=E;
 CC IsoId=Q92954-5; Sequence=VSP_016467, VSP_016470;
 CC Note=No experimental confirmation available;
 CC Name=F; Synonyms=Hemangiopoietin, HAP0;
 CC IsoId=Q92954-6; Sequence=VSP_016469;
 CC -!- TISSUE SPECIFICITY: Highly expressed in synovial tissue, cartilage
 CC and liver, and weakly in heart and lung. Isoform B is expressed in
 CC kidney, lung, liver, heart and brain. Isoform C and isoform D are
 CC widely expressed.
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: O-glycosylated; contains glycosaminoglycan chondroitin
 CC sulfate and keratan sulfate.
 CC -!- PTM: The disulfide bond between Cys-1146 and Cys-1403 is essential
 CC for protein cleavage (By similarity).
 CC -!- DISEASE: Defects in PRG4 are the cause of campodactyl-
 CC arthropathy-coxa vara-pericarditis syndrome (CACP) [MIM:208250];

CC also called Jacobs syndrome. CACP is an autosomal recessive
 CC disorder. Individuals with CACP have normal appearing joints at
 CC birth but with advancing age develop joint failure associated with
 CC noninflammatory synovioocyte hyperplasia and subintimal fibrosis of
 CC the synovial capsule.
 CC -1- MISCELLANEOUS: Different forms of various molecular weight have
 CC been observed. Such forms are possibly due to different levels of
 CC glycosylation and proteolysis cleavage (By similarity).
 CC -1- SIMILARITY: Contains 2 hemopexin-like domains.
 CC -1- SIMILARITY: Contains 2 SMR (somatomedin B) domains.
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 CC
 DR EMBL; U70136; AAB09089.1; -; mRNA.

Query Match 86.8%; Score 33; DB 1; Length 1404;
 Best Local Similarity 85.7%; Pred. No. 8.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 Db 1171 WMLSPFS 1177

RESULT 25
 Q46T11_RALEJ PRELIMINARY; PRT; 74 AA.
 AC Q46T11;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Hypothetical protein.
 GN OrderedLocNames=Reut_B4097;
 OS Ralstonia eutropha (strain JMP134) (Alcaligenes eutrophus).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Burkholderiaceae; Cupriavidus.
 CC NCBI_TaxID=264198;
 CC
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
 RA Hammon N., Istant S., Plick S., Goldsman B., Martinez M.,
 RA Schmutz J., Larimer F., Land M., Lykidis A., Richardson P.;
 RT "Complete sequence of chromosome 2 of Ralstonia eutropha JMP134.";
 RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.
 CC
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 CC
 DR EMBL; CP000091; AA263453.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 74 AA; 8424 MW; 39E3984BB7262AE CRC64;

Query Match 84.2%; Score 32; DB 2; Length 74;
 Best Local Similarity 71.4%; Pred. No. 67;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 Db 23 WMLAFA 29

RESULT 26
 Q4S8Z0_TESTNG PRELIMINARY; PRT; 117 AA.
 AC Q4S8Z0;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Chromosome 7 SCAR14703, whole genome shotgun sequence.
 GN ORNames=GSTENG00022129001;
 OS Tetraodon nigroviridis (Green puffer).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontidae; Tetraodon.
 CC NCBI_TaxID=99883;
 CC
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=15496914; DOI=10.1038/nature03025;
 RX Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dadiyva C., Salanoubat M., Levy M., Boudet N., Castellan S.,
 RA Anhouard V., Jabin C., Castelli V., Katinka M., Vacherie B.,
 RA Bismont C., Skalli Z., Cactolico L., Poullain J., De Bernardis V.,
 RA Crnaud C., Duprat S., Brotier P., Couanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Westrov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 CC
 RN NUCLEOTIDE SEQUENCE.
 RP Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC
 DR EMBL; CAE01014703; CAC02892.1; -; Genomic DNA.
 SQ SEQUENCE 117 AA; 12900 MW; 8D07018118BF483 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 117;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
 Db 30 WMLSAFS 36

RESULT 27
 Q43Q96_SOLUS PRELIMINARY; PRT; 129 AA.
 ID Q43Q96_SOLUS
 AC Q43Q96;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Transport-associated precursor.
 GN ORNames=AcidDRAFT_1152;
 OS Solibacter usitatus Ellin6076
 CC Bacteria; Acidobacteriales; Solibacteres; Solibacterales;
 CC Solibacteriaceae; Solibacter.
 CC NCBI_TaxID=234267;
 CC
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Ellin6076;
 RC US DOE Joint Genome Institute (JGI-RGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Istant S., Plick S., Goldsman B., Martinez M.,
 RA "Sequencing of the draft genome and assembly of Solibacter usitatus
 RT Ellin6076.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Ellin6076;
 RC US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Solibacter usitatus.";

```

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAI0100063; EAM54975.1; -; Genomic_DNA.
DR InterPro; IPR007055; TAD.
DR Pfam; PF04972; BON; 1.
DR PROSITE; PS50914; BON; 1.
DR Signal.
FT SIGNAL
SQ SEQUENCE 129 AA; 13518 MW; A7290632DFF510E4 CRC64;

Query March 84.2%; Score 32; DB 2; Length 129;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 2 WMLNAFT 8

RESULT 28
O9WXJ3 PORGI PRELIMINARY; PRT; 159 AA.
ID O9WXJ3 PORGI
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Dps.
GN Name=dps;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RX MEDLINE=22483669; PubMed=12595429;
RA DOI=10.1128/IAI.71.3.1170-1178.2003;
RA Ueshima J., Shoji M., Ratnayake D.B., Abe K., Yoshida S., Yamamoto K.,
RA Nakayama K.;
RA "Purification, gene cloning, gene expression, and mutants of Dps from
RT the obligate anaerobe Porphyromonas gingivalis.";
RL Infect. Immun. 71:1170-1178(2003).
CC -----
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CC -----
DR EMBL; AB025779; BAA76886.1; -; Genomic_DNA.
DR HSSP; Q8RP01; 1JIG.
DR GO; GO:0008199; F:ferriic iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR002177; Dps DNA bd.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR012347; Ferritin_rel.
DR Pfam; PF00210; Ferritin; 1.
DR PRINTS; PR01346; HELNAPAPROT.
DR PRODOM; PD149803; DPS; 1.
DR PROSITE; PS00818; DPS_1; 1.
DR PROSITE; PS00819; DPS_2; 1.
SQ SEQUENCE 159 AA; 17793 MW; 60889B904D33184C CRC64;

Query Match 84.2%; Score 32; DB 2; Length 159;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 2 WMLNAFT 8

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Db 151 WMLSAVA 157

RESULT 29
O7MXS1 PORGI PRELIMINARY; PRT; 159 AA.
ID O7MXS1 PORGI
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Dps family protein.
GN OrderedCusNames=PG0090; ORFNames=PG_0090;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RX MEDLINE=22829867; PubMed=12949112;
RA DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwim M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan W.C.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83."
RL J. Bacteriol. 185:5591-5601(2003).
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CC -----
DR EMBL; AE015924; AA065337.1; -; Genomic_DNA.
DR HSSP; Q8RP01; 1JIG.
DR TIGR; PG0090; -.
DR Biocyc; PGIN242619; PG0090-MONOMER; -.
DR GO; GO:0008199; F:ferriic iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR002177; Dps DNA bd.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR012347; Ferritin_rel.
DR Pfam; PF00210; Ferritin; 1.
DR PRINTS; PR01346; HELNAPAPROT.
DR PRODOM; PD149803; DPS; 1.
DR PROSITE; PS00818; DPS_1; 1.
DR PROSITE; PS00819; DPS_2; 1.
KM Complete proteome.
SQ SEQUENCE 159 AA; 17865 MW; 60889B904D331AC6 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 159;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 151 WMLSAVA 157

RESULT 30
O84S36 ORYSA PRELIMINARY; PRT; 167 AA.
ID O84S36 ORYSA
AC O84S36;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein OJ9990_A01.131 (Hypothetical protein
DE OJ1449_C01.14).
GN Name=OJ9990_A01.131; Synonyms=OJ1449_C01.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bp clade;

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OC Euhartioideae; Oryzaeae; Oryza.
RX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
clone:OJ9990 A01.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
clone:OJ1449 C01.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AP005847; BAC99919.1; -; Genomic DNA.
DR EMBL; AP005605; BAC99823.1; -; Genomic DNA.
DR Gramene; O84536; -.
KW Hypothetical protein.
SQ SEQUENCE 167 AA; 18427 MW; 367D8ABC62C1BB8 CRC64;

Query Match      84.2%; Score 32; DB 2; Length 167;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
   |||:|
   58 WMLAFA 64

RESULT 31
O4SFB2.TETNG PRELIMINARY; PRT; 182 AA.
ID O4SFB2.TETNG
AC O4SFB2;
DT 19-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUN-2005, sequence version 1.
DE Chromosome 6 SCAF14605, entry version 3.
GN ORNames=GSTENG00019173001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dastilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Udin C., Castelli V., Katinka M., Vacherie B.,
RA Bilemont C., Skalli Z., Catolico L., Poullain J., De Bernardis V.,
RA Parra G., Duprat S., Brotilier P., Coutanceau J.-P., Gouzy J.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croillius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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CC -----
DR EMBL; CAE01014605; CA00670.1; -; Genomic DNA.
SQ SEQUENCE 182 AA; 20009 MW; 0869B43C89CB7475 CRC64;

Query Match      84.2%; Score 32; DB 2; Length 182;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
   |||:|
   71 WMLAFA 77

RESULT 32
PUT2_FUGRU STANDARD; PRT; 187 AA.
ID PUT2_FUGRU
AC 07698;
DT 10-MAY-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Putative protein 2 (PUT2) (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Riboldi Tumiciliffe G.R., Platzer M., Nyakatura G., Elgar G.S.,
RA Brenner S., Rosenthal A.;
RT "Analysis of the genomic loci of Fugu rubripes homologs of the human
disease genes LiCAM, G6PD and P55.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (potential).
CC -!- SIMILARITY: Belongs to the TMEM9 family.
CC -----
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CC -----
DR EMBL; AF026198; AAC15584.1; -; Genomic DNA.
DR PIR; T30536; T30536.
DR Ensemble; SINFUD0000152263; Fugu rubripes.
DR GO; GO:0005770; C:late endosome; ISS.
DR GO; GO:0005764; C:lysosome; ISS.
DR InterPro; IPR004153; CXCXC_repeat.
DR InterPro; IPR008853; TMEM9.
DR PANTHER; PTHR13064; TMEM9; 1.
DR Pfam; PF03128; CXCXC; 1.
DR Pfam; PF05434; TMEM9; 1.
KW Hypothetical protein; Membrane; Transmembrane.
FT CHAIN 1 >187 Putative protein 2.
FT TRANSMEM 10 27 /FTId=PRO_0000221039.
FT TRANSMEM 99 121 Potential.
FT NON TER 187 187 Potential.
SQ SEQUENCE 187 AA; 21460 MW; 51DD101FB466DD3B CRC64;

Query Match      84.2%; Score 32; DB 1; Length 187;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
   |||:|
   9 WMLAFA 15

RESULT 33
O6CXD3_KLUNA

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ID OQCKD3_KLULA PRELIMINARY; PRT; 226 AA.
AC OQCKD3;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Similar to sp|P38869 Saccharomyces cerevisiae YHR181w singleton.
GN OrderedLocustNames=KLUA0A029255g;
OS Kluveromyces lactic (Yeast).
OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
OX NCBI_TaxID=26985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
RX PubMed:15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Talla E., Lafontaine I., de Montigny J., Marck C., Neveglies C., Talla E., Goffard N., Prangeul L., Aigle M., Anthouard V., Bahour A., Barbe V., Batnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C., Boissarie A., Boyer J., Catholico L., Confantolero F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicand J.-M., Nikolaki M., Ozas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J., Wincker P., Souciet J.-L.;
RA "Genome evolution in yeasts.";
RT Nature 430:35-44(2004).
RL -----
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CC -----
DR EMBL: CR382121; CAH02994.1; -; Genomic_DNA.
DR InterPro: IPR007277; DUF396.
DR PANTHER: PTHR13144; DUF396; 1.
DR Pfam: PF04148; DUF396; 1.
DR Complete proteome.
DR KW SEQUENCE 226 AA; 26133 MW; D45342F19A9CCEID CRC64;
SQ
Query Match 84.2%; Score 32; DB 2; Length 226;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 WMLSAFS 7
Db 66 WMLTAFS 72

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RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AK127961; BAC87208.1; -; mRNA.
DR HSSP: P16115; 1A5Z.
DR GO: GO:0004459; F:L-lactate dehydrogenase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR GO: GO:0006100; P:tricarboxylic acid cycle intermediate metab. .; IEA.
DR InterPro: IPR001557; L_IDH_NDH.
DR InterPro: IPR01304; L_IDH_NDH.
DR InterPro: IPR001236; lact_mal_DH.
DR InterPro: IPR002020; NAD_B5.
DR InterPro: IPR000594; Th1F_NAD_PAD_bd.
DR PANTHER: PTHR11540; Ldh; 1.
DR Pfam: PF02866; Ldh_1_C; 1.
DR Pfam: PF00056; Ldh_1_N; 1.
DR PRINTS: PR00086; LIDHDSGNASE.
DR PROSITE: PS00064; L_IDH; UNKNOWN 1.
DR SQ SEQUENCE 243 AA; 26419 MW; 98D3B92406208F25 CRC64;
SQ
Query Match 84.2%; Score 32; DB 2; Length 243;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 WMLSAFS 7
Db 187 WMLTAFS 193

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RESULT 35
P72049 MYCTU PRELIMINARY; PRT; 280 AA.
AC P72049; Q7D4V5;
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE PROBABLE O-ANTIGEN/LIPOPOLYSACCHARIDE TRANSPORT INTEGRAL MEMBRANE
DE PROTEIN ABC TRANSPORTER RPB2 (O-antigen export system, permease
DE protein).
GN Name=rfbD; OrderedLocustNames=WT3892, RV3783;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigemeier K., Gae S., Barry C.E. III,
RA Tekala F., Badcock K., Baaham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Fellwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J.E., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RA complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

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RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayan L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A.L., Uitterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishal W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
CC -----
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CC -----
DR EMBL: BX842584; CAB02462.1; -; Genomic DNA.
DR EMBL: AE000516; AK48257.1; -; Genomic DNA.
DR PIR: C70696; C70696.
DR TIGR: MT3892; -.
DR Tuberculist; RV3783; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000412; ABC_2.
DR Pfam: PF01061; ABC2_membrane; 1.
KM Complete proteome.
SQ SEQUENCE 280 AA; 32336 MW; D8793899C05A7EC3 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 262 WMLAFA 268

RESULT 36
O7TVN9_MYCBO PRELIMINARY; PRT; 280 AA.
AC O7TVN9;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE PROBABLE O-ANTIGEN/LIPOPOLYSACCHARIDE TRANSPORT INTEGRAL MEMBRANE
DE PROTEIN ABC TRANSPORTER RFBID.
GN Name=rfbD; OrderedLocustNames=MB3812;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1765;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
RA Puyot M., Dutfoy S., Grondin S., Lacroix C., Monsempre C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: BX248347; CAD95998.1; -; Genomic DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000412; ABC_2.
DR Pfam: PF01061; ABC2_membrane; 1.
KM Complete proteome.
SQ SEQUENCE 280 AA; 32336 MW; D8793899C05A7EC3 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 262 WMLAFA 268

RESULT 37
MRGRG_MOUSE STANDARD; PRT; 289 AA.
ID MRGRG_MOUSE
AC 091255; 0711N2;
DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Mas-related G-protein coupled receptor member G (Evolutionary
DE breakpoint transcript 2 protein).
GN Name=Mrgprg; Synonyms=Ebrt2, Mrgs;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=C57BL/6;
RX MEDLINE=21435808; PubMed=11551509; DOI=10.1016/S0092-8674(01)00483-4;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RT nociceptive sensory neurons.";
RL Cell 106:619-632(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 1-156.
RC STRAIN=C57BL/6;
RA Engemann S., Stroedicke M., Meguro M., Franck O., Kalscheuer V.,
RA Oshimura M., Walter J.;
RT "The BWS region contains an evolutionary breakpoint region.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Orphan receptor. May regulate nociceptor function and/or
CC development, including the sensation or modulation of pain.
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC Mas subfamily.
CC -----
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CC -----
DR EMBL: AY042212; AK91803.1; -; Genomic DNA.
DR EMBL: AJ313465; CAC86130.1; -; mRNA.
DR EMBL: ENSMUSG0000050276; Mus musculus.
DR MGI: MGI:3033145; Mrgprg.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE NEG.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; FALSE NEG.
KM G-protein coupled receptor; Membrane; Receptor; Transducer;
KM Transmembrane.
RL CHAIN 1 289
FT FT
FT member G.
FT /FTID=PRO_0000069768.
FT Extracellular (Potential).
FT 1 (Potential).
FT Cytoplasmic (Potential).
FT 2 (Potential).
FT Extracellular (Potential).
FT 3 (Potential).
FT Cytoplasmic (Potential).
FT 4 (Potential).
FT Extracellular (Potential).
FT 5 (Potential).
FT TRANSMEM 165 185

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FT TOPO_DOM 186 199 Cytoplasmic (Potential).
FT TRANSMEM 200 220 6 (Potential).
FT TOPO_DOM 221 222 Extracellular (Potential).
FT TRANSMEM 223 243 7 (Potential).
FT TOPO_DOM 244 289 Cytoplasmic (Potential).
FT CONFLICT 122 122 T->I (in Ref.2).
SQ SEQUENCE 289 AA; 32028 MW; 82BD4BEA02E0864C CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 1; Length 289;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 94 WMLAIFS 100

RESULT 38
O498A2_MOUSE PRELIMINARY; PRT; 289 AA.
ID O498A2_MOUSE PRELIMINARY; PRT; 289 AA.
AC Q498A2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE MAS-related GPR, member G.
GN Name=Mrgpr3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheef C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SOURCE/CELLULAR LOCATION: Membrane; multi-pass membrane protein (By
similarity).
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CC -----
CC EMBL, BC100302; AA100303.1; -, mRNA.
DR MGI; MGI:3033145; Mrgpr3.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.

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DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 289 AA; 32028 MW; 82BD4BEA02E0864C CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 289;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 94 WMLAIFS 100

RESULT 39
O3M9S1_ANAVY PRELIMINARY; PRT; 333 AA.
ID O3M9S1_ANAVY PRELIMINARY; PRT; 333 AA.
AC O3M9S1;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein precursor.
GN ORFNames=Ava_2652;
OS Anabaena variabilis (strain ATCC 29413).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=240292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 29413;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,
RA Hamon N., Istant S., Pittluck S., Saunders E.H., Schmutz J.,
RA Latimer F., Land M., Kyriades N., Savromatis K., Richardson P.;
RT "Complete sequence of Anabaena variabilis ATCC 29413";
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL, CP000117; AB22265.1; -, Genomic_DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1 29 Potential.
SQ SEQUENCE 333 AA; 37291 MW; 1F1E00BAF83097F3 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 333;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 17 WMLSSFS 23

RESULT 40
O2TNR7_9DIPT PRELIMINARY; PRT; 341 AA.
ID O2TNR7_9DIPT PRELIMINARY; PRT; 341 AA.
AC O2TNR7;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila unimaculata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=311483;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Matabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,

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RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
CC -----
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CC -----
DR EMBL: AY750084; AAX52015.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR Mitochondrion; NAD: Oxidoreductase; Ubiquinone.
FT NON TER 341 341
SQ SEQUENCE 341 AA; 39719 MW; 4754704028E5995A CRC64;

Query Match 84.2%; Score 32; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 185 WMLSALS 191

RESULT 41
Q2TNS2_9DIPT PRELIMINARY; PRT; 341 AA.
ID Q2TNS2_9DIPT
AC Q2TNS2_
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila mediocincta.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=311480;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
CC -----
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CC -----
DR EMBL: AY750079; AAX52010.1; -; Genomic_DNA.
DR EMBL: AY750074; AAX52005.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR Mitochondrion; Ubiquinone.
FT NON TER 341 341
SQ SEQUENCE 341 AA; 39472 MW; FCA6B7F94E90A733 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 185 WMLSALS 191

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AC Q2TNS6;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila mediocincta.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=311480;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
CC -----
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CC -----
DR EMBL: AY750069; AAX52000.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR Mitochondrion; NAD: Oxidoreductase; Ubiquinone.
FT NON TER 341 341
SQ SEQUENCE 341 AA; 39589 MW; A9B3CC084A3B5B95 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 185 WMLSALS 191

RESULT 43
Q2TNT2_9DIPT PRELIMINARY; PRT; 341 AA.
ID Q2TNT2_9DIPT
AC Q2TNT2_
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila trisana.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=65966;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
CC -----
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CC -----

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Query Match 84.2%; Score 32; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 185 WMLSALS 191

RESULT 44
Q2TNT3_9DIPT PRELIMINARY; PRT; 341 AA.
AC Q2TNT3;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila paramelanica.
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=311477;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
groups based on mitochondrial and nuclear DNA sequences."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).

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CC EMBL: AY750068; AAX5199.1; -!- Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 341 341
SQ SEQUENCE 341 AA; 39575 MW; 4A142BDA3BE5BD CRC64;

Query Match 84.2%; Score 32; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 185 WMLSALS 191

RESULT 45
Q2TNT5_9DIPT PRELIMINARY; PRT; 341 AA.
AC Q2TNT5;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila moritaki.
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=107829;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
groups based on mitochondrial and nuclear DNA sequences."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).

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CC EMBL: AY750065; AAX51996.1; -!- Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 341 341
SQ SEQUENCE 341 AA; 39646 MW; 5D1FDBA2786B4A5 CRC64;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).

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CC EMBL: AY750066; AAX51997.1; -!- Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 341 341
SQ SEQUENCE 341 AA; 39479 MW; 686D590B56FDE76A CRC64;

Query Match 84.2%; Score 32; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 185 WMLSALS 191

RESULT 46
Q2TNT6_9DIPT PRELIMINARY; PRT; 341 AA.
AC Q2TNT6;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE NADH dehydrogenase subunit 2 (Fragment).
OS Drosophila melanica.
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=189258;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
groups based on mitochondrial and nuclear DNA sequences."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).

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CC EMBL: AY750065; AAX51996.1; -!- Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
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Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 185 WMLSALS 191

RESULT 47
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AC Q2TNT7_DROMX;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.


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DE NADH dehydrogenase subunit 2 (Fragment).
OG Drosophila melanica (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7252;
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RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
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DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 341
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Db 185 WMLSAFS 191

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DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
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OG Mitochondrion.
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RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
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DT 24-JAN-2006, sequence version 1.
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RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
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DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
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OS Drosophila tsigana.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=65966;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang B.-C., Park J., Watabe H.-A., Gao J.-J., Aotsuka T., Chen H.-W.,
RA Zhang Y.-P.;
RT "Phylogenetic analysis of the Drosophila robusta and melanica species
RT groups based on mitochondrial and nuclear DNA sequences.";
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane;
CC multi-pass membrane protein (By similarity).
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Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
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Db 185 WMLSHLS 191
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Search completed: August 29, 2006, 06:13:05
Job time : 77 secs

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OM protein - protein search, using sw model

Run on: August 29, 2006, 06:14:29 ; Search time 12.0594 Seconds
(without alignments)
50.808 Million cell updates/sec

Title: US-10-541-343-3

Perfect score: 38

Sequence: 1 WHMARS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Issued Patents AA:*
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2: /EMC_Celerra_SIDS3/prodata/2/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	33	86.8	46	3	US-10-124-557-72
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24	33	86.8	46	3	US-07-757-022B-46
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133	28	73.7	1085	2	US-08-484-719B-5	Sequence 5, Appl1	206	27	71.1	996	2	US-10-101-464A-933	Sequence 933, App
134	28	73.7	1085	2	US-08-484-159-5	Sequence 5, Appl1	207	27	71.1	1001	1	US-07-797-556-6	Sequence 6, Appl1
135	28	73.7	1089	2	US-10-012-231A-102	Sequence 102, App	208	27	71.1	1001	1	US-07-943-843-2	Sequence 2, Appl1
136	28	73.7	1089	2	US-10-015-389A-102	Sequence 102, App	209	27	71.1	1001	1	US-08-347-003-2	Sequence 2, Appl1
137	28	73.7	1089	2	US-10-006-768A-102	Sequence 102, App	210	27	71.1	1097	1	US-07-943-843-6	Sequence 6, Appl1
138	28	73.7	1089	2	US-10-015-671A-102	Sequence 102, App	211	27	71.1	1097	1	US-08-347-003-6	Sequence 6, Appl1
139	28	73.7	1089	2	US-10-015-393A-102	Sequence 102, App	212	27	71.1	1097	2	US-09-949-016-6209	Sequence 6209, Ap
140	28	73.7	1089	2	US-10-011-833A-102	Sequence 102, App	213	27	71.1	1114	2	US-09-262-537-34	Sequence 34, Appl1
141	28	73.7	1089	2	US-10-006-041A-102	Sequence 102, App	214	27	71.1	1119	2	US-09-949-016-10081	Sequence 10081, A
142	28	73.7	1089	2	US-10-012-064A-102	Sequence 102, App	215	27	71.1	1133	2	US-09-262-537-4	Sequence 4, Appl1
143	28	73.7	1089	2	US-10-015-392A-102	Sequence 102, App	216	27	71.1	1143	2	US-09-538-092-3399	Sequence 399, App
144	28	73.7	1089	3	US-10-011-795B-102	Sequence 102, App	217	27	71.1	1177	2	US-09-262-537-2	Sequence 2, Appl1
145	28	73.7	1089	3	US-10-015-386A-102	Sequence 102, App	218	27	71.1	1207	2	US-09-927-112-2	Sequence 2, Appl1
146	28	73.7	1089	3	US-10-012-121A-102	Sequence 102, App	219	27	71.1	1224	2	US-09-930-872-4	Sequence 4, Appl1
147	28	73.7	1089	3	US-10-006-485A-102	Sequence 102, App	220	27	71.1	1224	2	US-10-217-777-4	Sequence 4, Appl1
148	28	73.7	1089	3	US-10-006-746A-102	Sequence 102, App	221	27	71.1	1224	2	US-09-262-537-6	Sequence 6, Appl1
149	28	73.7	1089	3	US-10-012-752A-102	Sequence 102, App	222	27	71.1	1703	2	US-09-824-574-3	Sequence 340, App
150	28	73.7	1089	3	US-10-017-253A-102	Sequence 102, App	223	27	71.1	1703	2	US-09-487-558B-340	Sequence 340, App
151	28	73.7	1089	3	US-10-015-519A-102	Sequence 102, App	224	27	71.1	141	1	US-08-311-611A-176	Sequence 176, App
152	28	73.7	1089	3	US-10-015-715A-102	Sequence 102, App	225	27	71.1	141	1	US-08-372-783-176	Sequence 176, App
153	28	73.7	1089	3	US-10-007-236A-102	Sequence 102, App	226	27	71.1	141	1	US-08-372-105-176	Sequence 176, App
154	28	73.7	1850	2	US-09-620-093A-5	Sequence 5, Appl1	227	27	71.1	141	1	US-08-306-473A-176	Sequence 176, App
155	28	73.7	2247	2	US-09-091-219-2	Sequence 2, Appl1	228	27	71.1	141	1	US-08-485-445A-176	Sequence 176, App
156	28	73.7	2247	2	US-09-660-541-2	Sequence 2, Appl1	229	27	71.1	141	1	US-08-621-259A-75	Sequence 75, Appl1
157	28	73.7	3340	2	US-09-252-991A-23568	Sequence 23568, A	230	27	71.1	141	2	US-09-119-2693-176	Sequence 176, App
158	27	71.1	69	2	US-09-621-976-5242	Sequence 5242, Ap	231	26	68.4	14	2	US-08-657-162-176	Sequence 176, App
159	27	71.1	69	2	US-09-621-976-5243	Sequence 5243, Ap	232	26	68.4	14	2	US-09-224-480-176	Sequence 176, App
160	27	71.1	70	2	US-09-270-767-60266	Sequence 60266, A	233	26	68.4	14	2	US-09-677-664B-75	Sequence 75, Appl1
161	27	71.1	71	2	US-09-134-000C-6365	Sequence 6365, Ap	234	26	68.4	14	2	US-09-689-097-173	Sequence 173, App
162	27	71.1	72	2	US-09-248-796A-25448	Sequence 25448, A	235	26	68.4	14	5	PCT-US95-00499-176	Sequence 176, App
163	27	71.1	75	2	US-09-621-976-4440	Sequence 4440, Ap	236	26	68.4	14	5	PCT-US95-00665-176	Sequence 176, App
164	27	71.1	115	2	US-10-104-047-3940	Sequence 3940, Ap	237	26	68.4	14	5	PCT-US95-09262-75	Sequence 75, Appl1
165	27	71.1	170	2	US-09-270-767-45761	Sequence 45761, Ap	238	26	68.4	15	2	US-09-255-501-136	Sequence 136, App
166	27	71.1	176	2	US-09-462-842-3	Sequence 3, Appl1	239	26	68.4	15	2	US-09-255-501-137	Sequence 137, App
167	27	71.1	176	2	US-09-393-171-3	Sequence 3, Appl1	240	26	68.4	15	2	US-09-255-501-138	Sequence 138, App
168	27	71.1	210	2	US-09-543-681A-8168	Sequence 8168, Ap	241	26	68.4	15	2	US-09-060-872A-137	Sequence 137, App
169	27	71.1	210	2	US-09-107-532A-4485	Sequence 4485, Ap	242	26	68.4	15	2	US-09-060-872A-137	Sequence 138, App
170	27	71.1	215	2	US-09-949-016-11620	Sequence 11620, A	243	26	68.4	15	2	US-09-060-872A-138	Sequence 136, App
171	27	71.1	229	2	US-09-252-991A-19517	Sequence 19517, A	244	26	68.4	15	2	US-09-500-135C-136	Sequence 137, App
172	27	71.1	269	2	US-09-902-540-10447	Sequence 10447, A	245	26	68.4	15	2	US-09-500-135C-137	Sequence 137, App

246	26	68.4	15	2	US-09-500-135C-138	Sequence 138, App	319	26	68.4	325	2	US-08-158-735A-13	Sequence 13, Appl
247	26	68.4	15	2	US-09-768-080-136	Sequence 136, App	320	26	68.4	329	2	US-09-270-767-42146	Sequence 42146, A
248	26	68.4	15	2	US-09-768-080-137	Sequence 137, App	321	26	68.4	331	2	US-09-603-208A-242	Sequence 242, App
249	26	68.4	15	2	US-09-768-080-138	Sequence 138, App	322	26	68.4	345	2	US-08-981-700A-5	Sequence 5, Appl
250	26	68.4	15	2	US-09-677-822A-136	Sequence 136, App	323	26	68.4	345	2	US-09-543-681A-7546	Sequence 7546, Ap
251	26	68.4	15	2	US-09-677-822A-137	Sequence 137, App	324	26	68.4	346	2	US-09-199-737-5	Sequence 5, Appl
252	26	68.4	15	2	US-09-677-822A-138	Sequence 138, App	325	26	68.4	346	2	US-08-993-088A-3	Sequence 3, Appl
253	26	68.4	18	2	US-09-407-687-14	Sequence 14, Appl	326	26	68.4	346	2	US-08-993-424B-3	Sequence 3, Appl
254	26	68.4	29	1	US-08-117-952-796	Sequence 796, App	327	26	68.4	346	2	US-09-058-333A-5	Sequence 5, Appl
255	26	68.4	61	2	US-09-621-976-5871	Sequence 5871, Ap	328	26	68.4	346	2	US-09-595-544-6	Sequence 6, Appl
256	26	68.4	60	2	US-09-134-000C-4340	Sequence 4340, Ap	329	26	68.4	346	2	US-08-899-112B-30	Sequence 30, Appl
257	26	68.4	72	2	US-09-248-796A-24979	Sequence 24979, A	330	26	68.4	346	2	US-09-011-553-7	Sequence 7, Appl
258	26	68.4	92	2	US-09-370-767-58901	Sequence 58901, A	331	26	68.4	346	3	US-10-007-132-5	Sequence 5, Appl
259	26	68.4	105	2	US-09-247-155-165	Sequence 165, App	332	26	68.4	347	2	US-09-489-039A-7810	Sequence 7810, Ap
260	26	68.4	108	2	US-09-903-190-165	Sequence 165, App	333	26	68.4	347	2	US-08-513-974B-46	Sequence 46, Appl
261	26	68.4	108	2	US-09-482-973-123	Sequence 123, App	334	26	68.4	348	2	US-08-513-974B-42	Sequence 342, App
262	26	68.4	140	2	US-09-949-016-6875	Sequence 6875, Ap	335	26	68.4	348	2	US-08-993-088A-10	Sequence 10, Appl
263	26	68.4	142	2	US-10-001-254-29	Sequence 29, App	336	26	68.4	348	2	US-08-993-424B-10	Sequence 10, Appl
264	26	68.4	147	2	US-09-540-236-3333	Sequence 3333, Ap	337	26	68.4	348	2	US-08-540-650B-2	Sequence 2, Appl
265	26	68.4	147	2	US-09-270-767-43535	Sequence 43535, A	338	26	68.4	348	2	US-09-595-548-5	Sequence 5, Appl
266	26	68.4	147	2	US-09-949-016-7124	Sequence 7124, Ap	339	26	68.4	348	2	US-09-661-435B-46	Sequence 46, Appl
267	26	68.4	162	2	US-09-252-991A-29190	Sequence 29190, A	340	26	68.4	348	2	US-09-603-680-10	Sequence 10, Appl
268	26	68.4	162	2	US-09-621-976-4128	Sequence 4128, Ap	341	26	68.4	349	2	US-08-513-974B-343	Sequence 343, App
269	26	68.4	174	2	US-09-270-767-46937	Sequence 46937, A	342	26	68.4	349	2	US-08-993-088A-11	Sequence 11, Appl
270	26	68.4	175	2	US-09-267-963D-32	Sequence 32, Appl	343	26	68.4	349	2	US-08-993-424B-11	Sequence 11, Appl
271	26	68.4	176	2	US-09-267-963D-31	Sequence 31, Appl	344	26	68.4	349	2	US-08-540-650B-5	Sequence 5, Appl
272	26	68.4	177	2	US-09-270-767-57414	Sequence 57414, A	345	26	68.4	349	2	US-08-693-308-2	Sequence 2, Appl
273	26	68.4	179	2	US-09-252-991A-24524	Sequence 24524, A	346	26	68.4	349	2	US-09-603-680-10	Sequence 10, Appl
274	26	68.4	181	2	US-09-902-540-9914	Sequence 9914, Ap	347	26	68.4	349	2	US-09-595-549-7	Sequence 7, Appl
275	26	68.4	182	2	US-09-267-963D-30	Sequence 30, Appl	348	26	68.4	349	2	US-09-603-680-11	Sequence 11, Appl
276	26	68.4	184	2	US-09-252-991A-19139	Sequence 19139, A	349	26	68.4	349	2	US-08-981-700A-6	Sequence 6, Appl
277	26	68.4	188	2	US-09-328-352-4862	Sequence 4862, Ap	350	26	68.4	349	2	US-09-826-509-503	Sequence 503, App
278	26	68.4	196	1	US-08-467-822-42	Sequence 42, Appl	351	26	68.4	351	2	US-08-513-974B-344	Sequence 344, App
279	26	68.4	196	2	US-09-107-383-11	Sequence 11, Appl	352	26	68.4	351	1	US-08-153-848-24	Sequence 24, Appl
280	26	68.4	196	2	US-08-432-697-42	Sequence 42, Appl	353	26	68.4	359	2	US-09-299-843A-24	Sequence 24, Appl
281	26	68.4	196	2	US-08-466-248-42	Sequence 42, Appl	354	26	68.4	359	2	US-09-336-378B-24	Sequence 24, Appl
282	26	68.4	196	2	US-09-742-361A-11	Sequence 11, Appl	355	26	68.4	359	2	US-09-336-643A-2	Sequence 2, Appl
283	26	68.4	197	2	US-09-489-039A-14194	Sequence 14194, A	356	26	68.4	359	5	PCR-US93-11153-24	Sequence 24, Appl
284	26	68.4	197	2	US-09-270-767-42732	Sequence 42732, A	357	26	68.4	375	1	US-08-946-875-8	Sequence 8, Appl
285	26	68.4	197	2	US-09-248-796A-26798	Sequence 26798, A	358	26	68.4	375	1	US-08-102-385G-8	Sequence 8, Appl
286	26	68.4	199	1	US-08-467-822-43	Sequence 43, Appl	359	26	68.4	378	2	US-09-299-843A-66	Sequence 66, Appl
287	26	68.4	199	2	US-08-432-697-43	Sequence 43, Appl	360	26	68.4	378	2	US-09-088-337B-66	Sequence 66, Appl
288	26	68.4	199	2	US-08-466-248-43	Sequence 43, Appl	361	26	68.4	384	2	US-09-949-016-9465	Sequence 9465, Ap
289	26	68.4	211	2	US-09-902-540-10687	Sequence 10687, A	362	26	68.4	395	2	US-08-900-230-5	Sequence 5, Appl
290	26	68.4	219	2	US-09-388-221B-21	Sequence 21, Appl	363	26	68.4	396	2	US-09-605-703B-1020	Sequence 1020, Ap
291	26	68.4	230	2	US-09-064-703-7	Sequence 7, Appl	364	26	68.4	396	2	US-09-605-703B-1022	Sequence 1022, Ap
292	26	68.4	235	2	US-09-345-236B-108	Sequence 108, App	365	26	68.4	413	2	US-09-684-855-142	Sequence 142, App
293	26	68.4	235	2	US-09-248-796A-15600	Sequence 15600, A	366	26	68.4	422	2	US-09-684-855-119	Sequence 119, App
294	26	68.4	241	2	US-09-489-039A-7888	Sequence 7888, Ap	367	26	68.4	422	2	US-09-488-265B-18	Sequence 18, Appl
295	26	68.4	246	2	US-09-270-767-44455	Sequence 44455, A	368	26	68.4	425	2	US-09-252-991A-17309	Sequence 17309, A
296	26	68.4	249	2	US-09-489-039A-9413	Sequence 9413, Ap	369	26	68.4	436	2	US-08-660-347-2	Sequence 2, Appl
297	26	68.4	255	2	US-09-248-796A-19627	Sequence 19627, A	370	26	68.4	442	2	US-08-993-359-28	Sequence 28, Appl
298	26	68.4	253	2	US-09-107-532A-7220	Sequence 7220, Ap	371	26	68.4	442	2	US-09-273-871A-4	Sequence 4, Appl
299	26	68.4	255	2	US-10-094-749-2763	Sequence 2763, Ap	372	26	68.4	442	2	US-09-482-558A-28	Sequence 28, Appl
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301	26	68.4	276	2	US-09-270-767-52463	Sequence 52463, A	374	26	68.4	443	2	US-09-603-208A-240	Sequence 240, App
302	26	68.4	279	2	US-09-134-000C-5300	Sequence 5300, Ap	375	26	68.4	444	2	US-09-328-352-476	Sequence 4726, Ap
303	26	68.4	280	2	US-09-255-501-209	Sequence 209, App	376	26	68.4	449	2	US-09-215-418-2	Sequence 2, Appl
304	26	68.4	280	2	US-09-060-872A-209	Sequence 209, App	377	26	68.4	452	2	US-09-107-532A-4860	Sequence 4860, Ap
305	26	68.4	280	2	US-09-500-135C-209	Sequence 209, App	378	26	68.4	454	2	US-09-134-000C-65335	Sequence 6535, Ap
306	26	68.4	280	2	US-09-768-080-209	Sequence 209, App	379	26	68.4	454	2	US-09-270-767-57120	Sequence 57120, A
307	26	68.4	280	2	US-09-677-822A-209	Sequence 209, App	380	26	68.4	470	3	US-09-886-954A-1	Sequence 1, Appl
308	26	68.4	281	2	US-09-973-278-172	Sequence 277, App	381	26	68.4	477	3	US-09-291-023A-2	Sequence 2, Appl
309	26	68.4	281	2	US-09-973-278-172	Sequence 277, App	382	26	68.4	485	2	US-09-291-023A-4	Sequence 4, Appl
310	26	68.4	281	2	US-09-252-991A-30174	Sequence 30174, A	383	26	68.4	485	2	US-09-291-023A-14	Sequence 14, Appl
311	26	68.4	293	2	US-10-014-269-31	Sequence 31, Appl	384	26	68.4	485	2	US-09-540-715A-2	Sequence 2, Appl
312	26	68.4	308	2	US-10-002-974-31	Sequence 31, Appl	385	26	68.4	485	2	US-09-540-715A-4	Sequence 4, Appl
313	26	68.4	308	2	US-08-981-957D-13	Sequence 13, Appl	386	26	68.4	485	2	US-09-540-715A-14	Sequence 14, Appl
314	26	68.4	314	2	US-09-982-704-13	Sequence 13, Appl	387	26	68.4	485	2	US-09-540-715A-15	Sequence 15, Appl
315	26	68.4	318	2	US-09-355-166-16	Sequence 16, Appl	388	26	68.4	485	2	US-09-540-715A-15	Sequence 15, Appl
316	26	68.4	320	2	US-09-248-796A-20977	Sequence 20977, A	389	26	68.4	485	2	US-09-540-715A-15	Sequence 15, Appl
317	26	68.4	320	2	US-09-248-796A-20977	Sequence 20977, A	390	26	68.4	485	2	US-09-540-715A-15	Sequence 15, Appl
318	26	68.4	323	2	US-08-158-735A-12	Sequence 12, Appl	391	26	68.4	493	2	US-09-949-016-7855	Sequence 7855, Ap

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393	26	68.4	510	2	US-08-476-123-4	Sequence 4, Appli	466	26	68.4	1052	2	US-09-500-105C-208	Sequence 208, App
394	26	68.4	510	2	US-09-742-684A-2	Sequence 4, Appli	467	26	68.4	1052	2	US-09-500-135C-208	Sequence 208, App
395	26	68.4	512	2	US-09-949-016-10977	Sequence 10977, A	468	26	68.4	1052	2	US-09-768-080-208	Sequence 208, App
396	26	68.4	513	1	US-08-357-533A-10	Sequence 10, Appl	469	26	68.4	1052	2	US-09-677-822A-208	Sequence 208, App
397	26	68.4	513	1	US-08-357-533A-11	Sequence 11, Appl	470	26	68.4	1194	2	US-09-949-016-10687	Sequence 10687, A
398	26	68.4	513	1	US-08-459-009-10	Sequence 11, Appl	471	26	68.4	1194	2	US-09-092-508-2	Sequence 2, Appli
399	26	68.4	513	1	US-08-459-009-11	Sequence 11, Appl	472	26	68.4	1194	2	US-09-435-115-2	Sequence 2, Appli
400	26	68.4	513	1	US-08-300-584-2	Sequence 2, Appli	473	26	68.4	1194	2	US-09-069-023-26	Sequence 26, Appli
401	26	68.4	513	1	US-08-459-951-10	Sequence 10, Appl	474	26	68.4	1194	2	US-09-098-310-2	Sequence 2, Appli
402	26	68.4	513	2	US-08-459-951-11	Sequence 11, Appl	475	26	68.4	1194	2	US-09-538-092-825	Sequence 825, App
403	26	68.4	513	2	US-08-738-168B-13	Sequence 13, Appl	476	26	68.4	1196	2	US-09-949-016-10065	Sequence 10065, Ap
404	26	68.4	513	2	US-08-476-123-2	Sequence 2, Appli	477	26	68.4	1196	2	US-09-949-016-10065	Sequence 10065, A
405	26	68.4	513	2	US-09-267-963D-34	Sequence 34, Appl	478	26	68.4	1196	2	US-09-949-016-10066	Sequence 10066, A
406	26	68.4	513	2	US-09-742-684A-2	Sequence 2, Appli	479	26	68.4	1205	2	US-09-092-508-16	Sequence 16, Appl
407	26	68.4	513	2	US-09-742-684A-16	Sequence 16, Appl	480	26	68.4	1205	2	US-09-435-115-16	Sequence 16, Appl
408	26	68.4	513	2	US-09-903-068C-30	Sequence 30, Appl	481	26	68.4	1239	2	US-09-949-016-6842	Sequence 6842, Ap
409	26	68.4	514	2	US-08-738-168B-15	Sequence 15, Appl	482	26	68.4	1239	2	US-09-949-016-10063	Sequence 10063, Ap
410	26	68.4	514	2	US-08-738-168B-15	Sequence 15, Appl	483	26	68.4	1239	2	US-09-949-016-10064	Sequence 10064, A
411	26	68.4	514	2	US-09-252-991A-25845	Sequence 25845, A	484	26	68.4	1236	2	US-08-857-636-60	Sequence 60, Appli
412	26	68.4	520	2	US-09-543-681A-5352	Sequence 5352, Ap	485	26	68.4	1236	5	PCT-US95-08354A-2	Sequence 60, Appli
413	26	68.4	521	2	US-09-252-991A-27089	Sequence 27089, A	486	26	68.4	1399	2	US-09-270-767-41876	Sequence 41876, A
414	26	68.4	521	2	US-08-738-168B-5	Sequence 5, Appli	487	26	68.4	1399	2	US-09-540-406-10	Sequence 10, Appl
415	26	68.4	536	1	US-08-357-533A-12	Sequence 12, Appl	488	26	68.4	1434	2	US-08-656-055-10	Sequence 10, Appl
416	26	68.4	536	1	US-08-459-009-12	Sequence 12, Appl	489	26	68.4	1434	2	US-08-656-055-10	Sequence 10, Appl
417	26	68.4	536	2	US-08-459-951-12	Sequence 12, Appl	490	26	68.4	1434	2	US-08-954-668-10	Sequence 10, Appl
418	26	68.4	536	2	US-09-267-963D-35	Sequence 35, Appl	491	26	68.4	1434	2	US-09-724-631-10	Sequence 10, Appl
419	26	68.4	536	2	US-09-903-068C-31	Sequence 31, Appl	492	26	68.4	1434	2	US-08-954-668-10	Sequence 10, Appl
420	26	68.4	543	2	US-09-949-016-7123	Sequence 7123, Ap	493	26	68.4	1434	2	US-09-949-016-6842	Sequence 6842, Ap
421	26	68.4	545	1	US-08-357-533A-9	Sequence 9, Appli	494	26	68.4	1434	2	US-09-949-016-10063	Sequence 10063, Ap
422	26	68.4	565	1	US-08-459-009-9	Sequence 9, Appli	495	26	68.4	1434	5	PCT-US95-13231-10	Sequence 10, Appl
423	26	68.4	567	1	US-08-361-873A-2	Sequence 2, Appli	496	26	68.4	1447	1	US-08-540-406-19	Sequence 19, Appl
424	26	68.4	567	1	US-08-483-926A-1	Sequence 1, Appli	497	26	68.4	1447	1	US-08-556-055-19	Sequence 19, Appl
425	26	68.4	567	1	US-08-854-768-1	Sequence 1, Appli	498	26	68.4	1447	2	US-08-954-668-19	Sequence 19, Appl
426	26	68.4	567	1	US-08-445-520B-9	Sequence 9, Appli	499	26	68.4	1447	2	US-09-268-140-5	Sequence 5, Appli
427	26	68.4	567	1	US-08-737-045-1	Sequence 1, Appli	500	26	68.4	1447	2	US-08-918-658-19	Sequence 19, Appl
428	26	68.4	567	2	US-08-451-946B-8	Sequence 8, Appli							
429	26	68.4	567	2	US-08-446-938B-8	Sequence 8, Appli							
430	26	68.4	567	2	US-08-311-703A-8	Sequence 8, Appli							
431	26	68.4	567	2	US-08-446-939B-8	Sequence 8, Appli							
432	26	68.4	567	2	US-09-183-543-8	Sequence 8, Appli							
433	26	68.4	567	2	US-08-446-936A-8	Sequence 8, Appli							
434	26	68.4	567	2	US-09-239-864A-11	Sequence 11, Appl							
435	26	68.4	567	2	US-09-878-905-11	Sequence 11, Appl							
436	26	68.4	567	2	US-09-267-963D-36	Sequence 36, Appl							
437	26	68.4	567	2	US-09-903-068C-32	Sequence 32, Appl							
438	26	68.4	567	5	PCT-US92-09326-4	Sequence 4, Appli							
439	26	68.4	573	2	US-09-540-236-2187	Sequence 2187, Ap							
440	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
441	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
442	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
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447	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
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452	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
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459	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
460	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
461	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
462	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
463	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							
464	26	68.4	580	2	US-09-949-016-8497	Sequence 8497, Ap							

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; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-3
; CURRENT APPLICATION NUMBER: US/09/592,018
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-592-018-4

Query Match      100.0%; Score 38; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
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        12 WMLSAFS 18

RESULT 3
US-09-989-481-4
; Sequence 4, Application US/09989481
; Patent No. 6841531
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-4
; CURRENT APPLICATION NUMBER: US/09/989,481
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 09/633,447
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-989-481-4

Query Match      100.0%; Score 38; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
        |||||
        12 WMLSAFS 18

RESULT 4
US-07-757-022B-18
; Sequence 18, Application US/07757022B
; Patent No. 6431142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
```

```

; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Gesner, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-18

Query Match      86.8%; Score 33; DB 2; Length 46;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
        |||||
        5 WMLSPFS 11

RESULT 5
US-10-124-557-18
; Sequence 18, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; APPLICANT: Clark, Stephen C.
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Gesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-124-557-18

Query Match 86.8%; Score 33; DB 3; Length 46;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 5 WMLSPFS 11

RESULT 6
US-07-757-022B-72
Sequence 72, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-72

Query Match 86.8%; Score 33; DB 2; Length 237;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 111 WMLSPFS 117

RESULT 7
US-10-124-557-72
Sequence 72, Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
APPLICANT: Clark, Stephen C.
APPLICANT: Jacobs, Kenneth
APPLICANT: Hewick, Rodney M.
APPLICANT: Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-124-557-72

Query Match 86.8%; Score 33; DB 3; Length 237;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 111 WMLSPFS 117

RESULT 8
US-07-757-022B-64
; Sequence 64, Application US/07757022B
; Patent No. 6431142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G1 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-07-757-022B-64

Query Match 86.8%; Score 33; DB 2; Length 372;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 139 WMLSPFS 145

RESULT 9
US-10-124-557-64
; Sequence 64, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; APPLICANT: Clark, Stephen C.
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Gesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G1 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-124-557-64

Query Match 86.8%; Score 33; DB 3; Length 372;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 139 WMLSPFS 145

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RESULT 10
US-07-757-022B-68
; Sequence 68, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-68

Query Match      86.8%; Score 33; DB 2; Length 422;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
; US-10-124-557-68

Query Match      86.8%; Score 33; DB 3; Length 422;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 WMLSAFS 7
Db      189 WMLSPFS 195

RESULT 11
US-10-124-557-68
; Sequence 68, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; APPLICANT: Clark, Stephen C.
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Gesner, Thomas G.
```

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RESULT 12
US-07-757-022B-66
; Sequence 66, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-66

Query Match 86.8%; Score 33; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPS 7
DB 190 WMLSPS 196

RESULT 13
US-10-124-557-66
Sequence 66; Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-124-557-66

Query Match 86.8%; Score 33; DB 3; Length 423;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPS 7
DB 190 WMLSPS 196

RESULT 14
US-07-757-022B-54
Sequence 54; Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
Clark, Stephen C.
Turner, Katherine
Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-54

Query Match 86.8%; Score 33; DB 2; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 230 WMLSPFS 236

RESULT 15
US-10-124-557-54
Sequence 54, Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-124-557-54

Query Match 86.8%; Score 33; DB 3; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 230 WMLSPFS 236

RESULT 16
US-07-757-022B-44
Sequence 44, Application US/07757022B
Patent No. 643142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
Clark, Stephen C.
APPLICANT: Turner, Katherine
Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-44

Query Match 86.8%; Score 33; DB 2; Length 1270;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 1037 WMLSPFS 1043

RESULT 17
US-10-124-557-44
; Sequence 44, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseerr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-124-557-44
Query Match 86.8%; Score 33; DB 3; Length 1270;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1037 WMLSPFS 1043

RESULT 18
US-07-757-022B-42
; Sequence 42, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseerr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-42
Query Match 86.8%; Score 33; DB 2; Length 1311;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1078 WMLSPFS 1084

RESULT 19
US-10-124-557-42
; Sequence 42, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42

Query Match 86.8%; Score 33; DB 3; Length 1311;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1078 WMLSPFS 1084

RESULT 20
US-07-757-022B-142
Sequence 142, Application US/07/57022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-142

Query Match 86.8%; Score 33; DB 2; Length 1313;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1080 WMLSPFS 1086

RESULT 21
US-10-124-557-142
Sequence 142, Application US/10/124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
APPLICANT: Clark, Stephen C.
APPLICANT: Jacobs, Kenneth
APPLICANT: Hewick, Rodney M.
APPLICANT: Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-124-557-142

Query Match 86.8%; Score 33; DB 3; Length 1313;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
DB 1080 WMLSPFS 1086

RESULT 22
US-07-757-022B-50
; Sequence 50, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Geener, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Geert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-50

Query Match 86.8%; Score 33; DB 2; Length 1314;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
DB 1081 WMLSPFS 1087

RESULT 23
US-10-124-557-50
; Sequence 50, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; APPLICANT: Clark, Stephen C.
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Geener, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Geert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50

Query Match 86.8%; Score 33; DB 3; Length 1314;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
DB 1081 WMLSPFS 1087

RESULT 24

US-07-757-022B-46
; Sequence 46, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine M.
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-46

Query Match 86.8%; Score 33; DB 2; Length 1320;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSPFS 7
Db 1087 WMLSPFS 1093

RESULT 25
US-07-757-022B-60
; Sequence 60, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine M.
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-60

Query Match 86.8%; Score 33; DB 2; Length 1320;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSPFS 7
Db 1087 WMLSPFS 1093

RESULT 26
US-10-164-595-58
; Sequence 58, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: IU 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 58
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-595-58

Query Match 86.8%; Score 33; DB 2; Length 1320;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1087 WMLSPFS 1093

RESULT 27

US-10-124-557-46
; Sequence 46, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseerr, Luanu
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-124-557-46

Query Match 86.8%; Score 33; DB 3; Length 1320;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1087 WMLSPFS 1093

RESULT 28
US-10-124-557-60
; Sequence 60, Application US/10124557
; Patent No. 7030223
; GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luanu
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-124-557-60

Query Match 86.8%; Score 33; DB 3; Length 1320;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1087 WMLSPFS 1093

RESULT 29
US-07-757-022B-48
; Sequence 48, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-48

Query Match 86.8%; Score 33; DB 2; Length 1354;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 1121 WMLSPFS 1127

RESULT 30
US-10-124-557-48
Sequence 48, Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-124-557-48

Query Match 86.8%; Score 33; DB 3; Length 1354;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 1121 WMLSPFS 1127

RESULT 31
US-07-757-022B-40
Sequence 40, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
APPLICANT: Turner, Katherine
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-40

Query Match 86.8%; Score 33; DB 2; Length 1361;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 1128 WMLSPFS 1134

RESULT 32
US-10-124-557-40
Sequence 40, Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-124-557-40

Query Match 86.8%; Score 33; DB 3; Length 1361;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 1128 WMLSPFS 1134

RESULT 33
US-07-757-022B-52
Sequence 52, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-52

Query Match 86.8%; Score 33; DB 2; Length 1363;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1130 WMLSPFS 1136

RESULT 34

US-10-124-557-52
Sequence 52, Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-124-557-52

Query Match 86.8%; Score 33; DB 3; Length 1363;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1130 WMLSPFS 1136

RESULT 35
US-07-757-022B-2
Sequence 2, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.

APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-2

Query Match 86.8%; Score 33; DB 2; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

RESULT 36
US-07-757-022B-62
Sequence 62, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts

```

; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-62

Query Match      86.8%; Score 33; DB 2; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
Db      1171 WMLSPFS 1177

RESULT 37
US-10-164-595-78
; Sequence 78, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: IU 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 78
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-595-78

Query Match      86.8%; Score 33; DB 2; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
Db      1171 WMLSPFS 1177
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RESULT 38
US-09-298-970A-1
; Sequence 1, Application US/09298970A
; Patent No. 6743774
; GENERAL INFORMATION:
; APPLICANT: Jay, Gregory D.
; TITLE OF INVENTION: TRIBONECTINS
; FILE REFERENCE: 21486-026
; CURRENT APPLICATION NUMBER: US/09/298,970A
; CURRENT FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-298-970A-1

Query Match      86.8%; Score 33; DB 2; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
Db      1171 WMLSPFS 1177

RESULT 39
US-09-897-188-1
; Sequence 1, Application US/09897188
; Patent No. 6960562
; GENERAL INFORMATION:
; APPLICANT: Jay, Gregory D.
; TITLE OF INVENTION: Tribonectin Polypeptides and Uses Thereof
; FILE REFERENCE: 21486-026 CIP2
; CURRENT APPLICATION NUMBER: US/09/897,188
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 09/298,970
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 09/556,246
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-897-188-1

Query Match      86.8%; Score 33; DB 2; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
Db      1171 WMLSPFS 1177

RESULT 40
US-09-556-246-1
; Sequence 1, Application US/09556246
; Patent No. 7001881
; GENERAL INFORMATION:
; APPLICANT: Gregory D. Jay
; TITLE OF INVENTION: tribonectins
; FILE REFERENCE: 21486-026CIP
; CURRENT APPLICATION NUMBER: US/09/556,246
; CURRENT FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: USSN 09/298/970
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 1
LENGTH: 1404
TYPE: PRT
ORGANISM: Homo sapiens
US-09-556-246-1

Query Match 86.8%; Score 33; DB 3; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

RESULT 41

US-10-124-557-2
Sequence 2, Application US/10124557
Patent No. 7030223

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:

NAME: Cserr, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: GI 5190

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1404 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-124-557-2

Query Match 86.8%; Score 33; DB 3; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

RESULT 42

US-10-124-557-62
Sequence 62, Application US/10124557
Patent No. 7030223

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:

NAME: Cserr, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: GI 5190

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 1404 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 62:

US-10-124-557-62

Query Match 86.8%; Score 33; DB 3; Length 1404;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

RESULT 43

US-09-949-016-10827
Sequence 10827, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10827
LENGTH: 1411
TYPE: PRT
ORGANISM: Human
US-09-949-016-10827

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 1411;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1178 WMLSPFS 1184

RESULT 44
US-09-107-532A-4889
Sequence 4889, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4889:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...103
SEQUENCE DESCRIPTION: SEQ ID NO: 4889:
US-09-107-532A-4889

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 103;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAF 6
Db 17 WMLSAF 22

RESULT 45
US-09-252-991A-22359
Sequence 22359, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22359
LENGTH: 262
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: UNSURE
LOCATION: (182)
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-22359

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 262;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 234 WMLSAIS 240

RESULT 46
US-09-712-363-283
Sequence 283, Application US/09712363
Patent No. 6892139
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward W.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093

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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-283

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 280;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 262 WMLAFA 268

RESULT 47
US-09-489-039A-7403
; Sequence 7403, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 66/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7403
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7403

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 437;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 391 WMLSAFS 397

RESULT 48
US-09-586-106D-99
; Sequence 99, Application US/09586106D
; Patent No. 6720479
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; APPLICANT: Voytas, Daniel F.
; TITLE OF INVENTION: PLANT RETROELEMENTS AND METHODS RELATED THERETO
; FILE REFERENCE: P-1065A
; CURRENT APPLICATION NUMBER: US/09/586,106D
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/087,125
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/322,478
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 229
; TYPE: PRT
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; ORGANISM: Lycopodium esculentum
US-09-586-106D-99

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 229;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 144 WMLSAFS 150

RESULT 49
US-10-799-870-99
; Sequence 99, Application US/10799870
; Patent No. 6949695
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; APPLICANT: Voytas, Daniel F.
; TITLE OF INVENTION: PLANT RETROELEMENTS AND METHODS RELATED THERETO
; FILE REFERENCE: P-1065A
; CURRENT APPLICATION NUMBER: US/10/799,870
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/586,106
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/087,125
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/322,478
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Lycopodium esculentum
US-10-799-870-99

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 229;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 144 WMLSAFS 150

RESULT 50
US-09-107-532A-3700
; Sequence 3700, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCIT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
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APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3700:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...119
SEQUENCE DESCRIPTION: SEQ ID NO: 3700:
US-09-107-532A-3700

Query Match 78.9%; Score 30; DB 2; Length 119;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
|||:|||
Db 11 WMTSFS 17

Search completed: August 29, 2006, 06:17:48
Job time : 17.0594 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 29, 2006, 09:58:08 ; Search time 84.6931 Seconds
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(without alignments)

Title: US-10-541-343-3

Perfect score: 38

Sequence: 1 WHLSARS 7

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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Published Applications AA Main:*

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- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	38	100.0	33	3	US-09-989-481-4
4	38	100.0	33	5	US-10-858-545-4
5	38	100.0	33	5	US-10-858-286-4
6	38	100.0	33	5	US-10-858-543-4
7	38	100.0	33	5	US-10-858-144-4
8	38	100.0	33	5	US-10-541-343-1
9	35	92.1	1760	6	US-11-097-143-16893
10	34	89.5	103	4	US-10-424-599-187845
11	33	86.8	46	6	US-10-124-557-18
12	33	86.8	46	6	US-11-169-332-18
13	33	86.8	61	3	US-09-925-301-1452
14	33	86.8	237	6	US-10-124-557-72
15	33	86.8	237	6	US-11-169-332-72
16	33	86.8	372	4	US-10-124-557-64
17	33	86.8	372	6	US-11-169-332-64
18	33	86.8	422	6	US-10-124-557-68
19	33	86.8	422	6	US-11-169-332-68
20	33	86.8	423	6	US-10-124-557-66
21	33	86.8	423	6	US-11-169-332-66
22	33	86.8	463	4	US-10-124-557-54
23	33	86.8	463	6	US-11-169-332-54
24	33	86.8	538	4	US-10-038-694-4
25	33	86.8	792	3	US-09-802-207-27
26	33	86.8	1046	4	US-10-425-115-37015
27	33	86.8	1270	4	US-10-124-557-44

28	33	86.8	1270	6	US-11-169-232-44	Sequence 44, Appl
29	33	86.8	1311	4	US-10-124-557-42	Sequence 42, Appl
30	33	86.8	1311	6	US-11-169-232-42	Sequence 42, Appl
31	33	86.8	1313	4	US-10-124-557-142	Sequence 142, Appl
32	33	86.8	1313	6	US-11-169-232-142	Sequence 142, Appl
33	33	86.8	1314	4	US-10-124-557-50	Sequence 50, Appl
34	33	86.8	1314	6	US-11-169-232-50	Sequence 50, Appl
35	33	86.8	1320	4	US-10-124-557-46	Sequence 46, Appl
36	33	86.8	1320	6	US-10-124-557-46	Sequence 46, Appl
37	33	86.8	1320	5	US-10-124-557-60	Sequence 60, Appl
38	33	86.8	1320	6	US-11-169-232-46	Sequence 46, Appl
39	33	86.8	1320	6	US-11-169-232-60	Sequence 60, Appl
40	33	86.8	1354	4	US-10-124-557-48	Sequence 48, Appl
41	33	86.8	1354	6	US-11-169-232-48	Sequence 48, Appl
42	33	86.8	1361	4	US-10-124-557-40	Sequence 40, Appl
43	33	86.8	1361	6	US-11-169-232-40	Sequence 40, Appl
44	33	86.8	1363	4	US-10-124-557-52	Sequence 52, Appl
45	33	86.8	1363	6	US-11-169-232-52	Sequence 52, Appl
46	33	86.8	1404	3	US-09-802-207-30	Sequence 30, Appl
47	33	86.8	1404	3	US-09-897-188-1	Sequence 1, Appl
48	33	86.8	1404	4	US-10-124-557-2	Sequence 2, Appl
49	33	86.8	1404	4	US-10-124-557-62	Sequence 62, Appl
50	33	86.8	1404	5	US-10-858-595-1	Sequence 1, Appl
51	33	86.8	1404	5	US-10-868-577A-55	Sequence 55, Appl
52	33	86.8	1404	5	US-10-717-665-78	Sequence 78, Appl
53	33	86.8	1404	6	US-11-169-232-2	Sequence 2, Appl
54	33	86.8	1404	6	US-11-169-232-62	Sequence 62, Appl
55	33	86.8	211	3	US-09-791-932-97	Sequence 97, Appl
56	33	86.8	211	5	US-10-980-388-97	Sequence 97, Appl
57	33	86.8	280	3	US-09-712-363-283	Sequence 283, Appl
58	33	86.8	289	4	US-10-407-960-2	Sequence 2, Appl
59	33	86.8	323	3	US-09-791-932-119	Sequence 119, Appl
60	33	86.8	323	4	US-10-332-156-119	Sequence 1, Appl
61	33	86.8	323	5	US-10-860-388-119	Sequence 1, Appl
62	33	86.8	371	4	US-10-471-115-1	Sequence 1, Appl
63	33	86.8	465	5	US-10-626-832-25	Sequence 25, Appl
64	33	86.8	511	4	US-10-437-963-120104	Sequence 120104, Appl
65	33	86.8	561	5	US-10-505-486-107	Sequence 107, Appl
66	33	86.8	623	4	US-10-437-963-144350	Sequence 144350, Appl
67	33	86.8	747	4	US-10-437-963-144356	Sequence 144356, Appl
68	33	86.8	1100	4	US-10-437-963-178971	Sequence 178971, Appl
69	33	86.8	1923	5	US-10-450-763-51701	Sequence 51701, Appl
70	33	86.8	76	3	US-09-764-891-3265	Sequence 3265, Appl
71	33	86.8	76	5	US-10-501-282-3808	Sequence 3808, Appl
72	33	86.8	77	4	US-10-424-599-184690	Sequence 184690, Appl
73	33	86.8	85	4	US-10-424-599-249435	Sequence 249435, Appl
74	33	86.8	91	4	US-10-001-857-125	Sequence 125, Appl
75	33	86.8	93	4	US-10-425-115-309566	Sequence 309566, Appl
76	33	86.8	99	4	US-10-425-115-260762	Sequence 260762, Appl
77	33	86.8	104	4	US-10-424-599-242038	Sequence 242038, Appl
78	33	86.8	133	4	US-10-425-115-193472	Sequence 193472, Appl
79	33	86.8	146	3	US-09-925-297-643	Sequence 643, Appl
80	33	86.8	148	3	US-10-678-786-30	Sequence 30, Appl
81	33	86.8	148	4	US-10-678-786-30	Sequence 30, Appl
82	33	86.8	163	4	US-10-767-770-59679	Sequence 59679, Appl
83	33	86.8	165	4	US-10-425-115-331668	Sequence 331668, Appl
84	33	86.8	178	4	US-10-156-761-7648	Sequence 7648, Appl
85	33	86.8	182	4	US-10-425-115-213595	Sequence 213595, Appl
86	33	86.8	186	4	US-10-425-115-213624	Sequence 213624, Appl
87	33	86.8	211	4	US-10-425-115-217396	Sequence 217396, Appl
88	33	86.8	229	4	US-10-395-607-99	Sequence 99, Appl
89	33	86.8	229	4	US-10-799-870-99	Sequence 99, Appl
90	33	86.8	253	3	US-09-888-615-96	Sequence 96, Appl
91	33	86.8	253	6	US-11-037-443-96	Sequence 96, Appl
92	33	86.8	302	4	US-10-425-115-213613	Sequence 213613, Appl
93	33	86.8	305	4	US-10-425-115-43471	Sequence 43471, Appl
94	33	86.8	322	4	US-10-424-599-241141	Sequence 241141, Appl
95	33	86.8	352	6	US-11-097-143-38151	Sequence 38151, Appl
96	33	86.8	371	3	US-09-981-900B-14	Sequence 14, Appl
97	33	86.8	373	4	US-10-425-115-211851	Sequence 211851, Appl
98	33	86.8	633	4	US-10-437-963-111838	Sequence 111838, Appl
99	33	86.8	41	5	US-10-948-571-77	Sequence 77, Appl
100	33	86.8	50	4	US-10-029-386-29222	Sequence 29222, Appl

101	30	78.9	51	6	US-11-096-568A-27324	Sequence 27324, A	174	29	76.3	127	3	US-09-933-767-438	Sequence 438, App
102	30	78.9	60	4	US-10-425-115-357009	Sequence 357009, A	175	29	76.3	127	4	US-10-004-860-438	Sequence 438, App
103	30	78.9	71	4	US-10-437-963-023604	Sequence 203604, A	176	29	76.3	137	4	US-10-023-282-438	Sequence 438, App
104	30	78.9	74	4	US-10-424-599-176425	Sequence 176425, A	177	29	76.3	128	4	US-10-425-115-246890	Sequence 246890, A
105	30	78.9	83	4	US-10-767-701-39437	Sequence 39437, A	178	29	76.3	121	4	US-10-437-963-203799	Sequence 203799, A
106	30	78.9	85	4	US-10-437-963-132576	Sequence 132576, A	179	29	76.3	116	4	US-10-282-122A-46540	Sequence 46540, A
107	30	78.9	126	4	US-10-425-115-559538	Sequence 259538, A	180	29	76.3	144	4	US-10-767-701-465747	Sequence 465747, A
108	30	78.9	152	3	US-09-974-879-608	Sequence 408, App	181	29	76.3	144	6	US-11-079-463-9208	Sequence 9208, App
109	30	78.9	152	3	US-09-305-736-408	Sequence 408, App	182	29	76.3	177	4	US-10-767-701-465904	Sequence 46904, A
110	30	78.9	152	3	US-09-818-683-408	Sequence 408, App	183	29	76.3	185	5	US-10-719-993-556	Sequence 556, App
111	30	78.9	152	3	US-09-818-683-408	Sequence 408, App	184	29	76.3	166	4	US-10-425-114-53586	Sequence 53586, A
112	30	78.9	152	3	US-10-621-401-192	Sequence 408, App	185	29	76.3	214	4	US-10-425-115-300451	Sequence 300451, A
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114	30	78.9	174	3	US-09-974-879-192	Sequence 192, App	187	29	76.3	233	4	US-10-335-977-5070	Sequence 5070, App
115	30	78.9	174	3	US-09-305-736-192	Sequence 192, App	188	29	76.3	220	5	US-10-873-467-36	Sequence 36, App
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118	30	78.9	174	3	US-10-621-401-192	Sequence 192, App	191	29	76.3	210	6	US-11-188-298-4579	Sequence 4579, App
119	30	78.9	179	4	US-10-767-701-54862	Sequence 54862, A	192	29	76.3	222	2	US-08-834-705-14	Sequence 14, App
120	30	78.9	182	4	US-10-369-493-5876	Sequence 5876, App	193	29	76.3	229	2	US-10-335-977-5071	Sequence 5071, App
121	30	78.9	267	5	US-10-732-923-16550	Sequence 16550, A	194	29	76.3	239	4	US-10-450-763-37146	Sequence 37146, A
122	30	78.9	267	5	US-10-732-923-16551	Sequence 16551, A	195	29	76.3	303	4	US-10-216-209-20	Sequence 20, App
123	30	78.9	267	6	US-11-188-288-20218	Sequence 20218, A	196	29	76.3	303	4	US-10-216-209-91	Sequence 91, App
124	30	78.9	268	6	US-11-188-288-1175	Sequence 1175, App	197	29	76.3	311	6	US-11-079-463-8727	Sequence 8727, App
125	30	78.9	273	4	US-10-369-493-3391	Sequence 3391, App	198	29	76.3	335	4	US-10-424-599-179218	Sequence 179218, App
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135	30	78.9	736	4	US-10-425-114-39293	Sequence 39293, A	208	29	76.3	335	4	US-10-006-807A-130	Sequence 130, App
136	30	78.9	761	6	US-11-188-298-18068	Sequence 18068, A	209	29	76.3	335	4	US-10-013-907A-130	Sequence 130, App
137	30	78.9	818	4	US-10-425-114-41341	Sequence 41341, A	210	29	76.3	335	4	US-10-015-499A-130	Sequence 130, App
138	30	78.9	832	4	US-10-424-599-254916	Sequence 254916, A	211	29	76.3	335	4	US-10-232-224-170	Sequence 170, App
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140	30	78.9	837	4	US-10-425-115-345033	Sequence 345033, A	213	29	76.3	335	4	US-10-216-159A-170	Sequence 170, App
141	30	78.9	844	5	US-10-732-923-8376	Sequence 8376, App	214	29	76.3	335	4	US-10-015-869A-130	Sequence 130, App
142	30	78.9	847	5	US-10-732-923-8521	Sequence 8521, App	215	29	76.3	335	4	US-10-012-121A-130	Sequence 130, App
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144	30	78.9	907	6	US-11-097-143-15312	Sequence 15312, A	217	29	76.3	335	4	US-10-227-873-170	Sequence 170, App
145	30	78.9	1087	4	US-10-437-963-129691	Sequence 129691, A	218	29	76.3	335	4	US-10-227-883-170	Sequence 170, App
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148	30	78.9	1769	4	US-10-361-522-3	Sequence 3, App	221	29	76.3	335	4	US-10-006-116A-130	Sequence 130, App
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150	30	78.9	4025	5	US-10-437-963-193926	Sequence 193926, A	223	29	76.3	335	4	US-10-017-527A-130	Sequence 130, App
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155	29	76.3	65	4	US-10-424-599-161491	Sequence 161491, A	228	29	76.3	335	4	US-10-219-466-170	Sequence 170, App
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158	29	76.3	77	4	US-10-335-977-8349	Sequence 8349, App	231	29	76.3	335	4	US-10-230-260-170	Sequence 170, App
159	29	76.3	79	4	US-10-767-701-46821	Sequence 46821, A	232	29	76.3	335	4	US-10-232-231-170	Sequence 170, App
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164	29	76.3	91	4	US-10-424-599-328363	Sequence 328363, A	237	29	76.3	335	4	US-10-218-956-170	Sequence 170, App
165	29	76.3	92	4	US-10-425-115-246899	Sequence 246899, A	238	29	76.3	335	4	US-10-219-468-170	Sequence 170, App
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170	29	76.3	114	3	US-09-892-877-160	Sequence 160, App	243	29	76.3	335	4	US-10-012-755A-130	Sequence 130, App
171	29	76.3	117	4	US-10-425-114-61328	Sequence 61328, A	244	29	76.3	335	4	US-10-219-072-170	Sequence 170, App
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248	29	76.3	335	4	US-10-219-528-170	Sequence 170, App	321	29	76.3	335	4	US-10-017-867A-130	Sequence 130, App
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308	29	76.3	335	4	US-10-015-591A-130	Sequence 130, App	381	29	76.3	335	5	US-10-012-149A-130	Sequence 130, App
309	29	76.3	335	4	US-10-223-089-190	Sequence 190, App	382	29	76.3	335	5	US-10-233-134-170	Sequence 170, App
310	29	76.3	335	4	US-10-017-407A-130	Sequence 130, App	383	29	76.3	335	5	US-10-219-062-170	Sequence 170, App
311	29	76.3	335	4	US-10-011-833A-130	Sequence 130, App	384	29	76.3	335	5	US-10-219-064-170	Sequence 170, App
312	29	76.3	335	4	US-10-006-041A-130	Sequence 130, App	385	29	76.3	335	5	US-10-218-784-170	Sequence 170, App
313	29	76.3	335	4	US-10-015-822A-130	Sequence 130, App	386	29	76.3	335	5	US-10-219-061-170	Sequence 170, App
314	29	76.3	335	4	US-10-015-387A-130	Sequence 130, App	387	29	76.3	335	6	US-11-025-607-130	Sequence 170, App
315	29	76.3	335	4	US-10-006-130A-130	Sequence 130, App	388	29	76.3	335	5	US-10-739-930-10040	Sequence 10040, A
316	29	76.3	335	4	US-10-216-163-170	Sequence 170, App	389	29	76.3	335	6	US-11-096-568A-25553	Sequence 25553, A
317	29	76.3	335	4	US-10-006-172A-130	Sequence 130, App	390	29	76.3	336	6	US-11-045-004-552	Sequence 552, A
318	29	76.3	335	4	US-10-017-253A-130	Sequence 130, App	391	29	76.3	337	4	US-10-767-701-46915	Sequence 46915, A
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393	29	76.3	357	4	US-10-425-115-246902
392	29	76.3	357	4	US-10-425-115-246905
391	29	76.3	357	4	US-10-425-115-246931
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413	29	76.3	449	4	US-10-425-115-338548
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416	29	76.3	500	6	US-11-079-463-5773
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427	29	76.3	810	5	US-10-723-860-1747
428	29	76.3	810	5	US-10-756-148-5159
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442	29	76.3	1818	4	US-10-032-588-7516
443	29	76.3	1878	6	US-11-097-143-13348
444	29	76.3	2005	5	US-10-450-763-154823
445	29	76.3	4101	4	US-10-369-493-6509
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447	29	76.3	4928	4	US-10-329-148A-5
448	28	73.7	25	4	US-10-029-298-27689
449	28	73.7	29	4	US-10-425-115-205847
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Sequence 22, App1
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Sequence 338548,
Sequence 314, App
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Sequence 180356,
Sequence 4055, Ap
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467	28	73.7	70	4	US-10-425-115-307311	Sequence 307311,
468	28	73.7	71	4	US-10-335-977-93071	Sequence 93071, Ap
469	28	73.7	75	3	US-09-864-761-45039	Sequence 45039, Ap
470	28	73.7	75	4	US-10-335-977-9308	Sequence 9308, Ap
471	28	73.7	77	4	US-10-425-115-299471	Sequence 299471,
472	28	73.7	80	3	US-09-989-890-194	Sequence 194, App
473	28	73.7	82	4	US-10-425-115-266020	Sequence 266020,
474	28	73.7	83	4	US-10-425-115-266021	Sequence 266021,
475	28	73.7	86	4	US-10-424-599-249255	Sequence 249255,
476	28	73.7	89	4	US-10-002-344-168	Sequence 168, App
477	28	73.7	89	5	US-10-958-862-168	Sequence 168, App
478	28	73.7	90	4	US-10-424-599-218746	Sequence 218746,
479	28	73.7	98	4	US-10-115-479-24	Sequence 24, Appl
480	28	73.7	100	4	US-10-029-386-28417	Sequence 28417, A
481	28	73.7	103	3	US-09-833-245-1395	Sequence 1395, Ap
482	28	73.7	103	3	US-09-833-245-1396	Sequence 1396, Ap
483	28	73.7	103	4	US-10-034-749-2935	Sequence 2935, Ap
484	28	73.7	103	6	US-11-264-096-1395	Sequence 1395, Ap
485	28	73.7	103	6	US-11-264-096-1396	Sequence 1396, Ap
486	28	73.7	105	4	US-10-437-963-124659	Sequence 124659, A
487	28	73.7	105	6	US-11-096-568A-23057	Sequence 23057, A
488	28	73.7	108	3	US-09-867-850-278	Sequence 278, App
489	28	73.7	109	4	US-10-437-863-168710	Sequence 168710,
490	28	73.7	114	4	US-10-424-599-328283	Sequence 328283,
491	28	73.7	116	4	US-10-424-599-230737	Sequence 230737,
492	28	73.7	122	4	US-10-424-599-230697	Sequence 230697,
493	28	73.7	124	6	US-11-096-568A-23056	Sequence 23056, A
494	28	73.7	126	4	US-10-437-963-200586	Sequence 200586,
495	28	73.7	127	4	US-10-767-701-33318	Sequence 33318, A
496	28	73.7	136	4	US-10-425-115-304184	Sequence 304184,
497	28	73.7	140	4	US-10-425-115-294547	Sequence 294547,
498	28	73.7	141	4	US-10-767-701-39126	Sequence 39126, A
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ALIGNMENTS

RESULT 1

US-10-541-343-3

Sequence 3, Application US/10541343

Publication No. US20060052299A1

GENERAL INFORMATION:

APPLICANT: Chau, Raymond Ming Wah

APPLICANT: Ko, Rui-Yuk Dorothy

TITLE OF INVENTION: NMTF Peptides and Compositions and Methods of Use

FILE REFERENCE: 2001-1030US

CURRENT APPLICATION NUMBER: US/10/541.343

CURRENT FILING DATE: 2005-07-05

PRIOR APPLICATION NUMBER: PCT/US2004/001468

PRIOR FILING DATE: 2004-01-21

PRIOR APPLICATION NUMBER: 60/441,722

PRIOR FILING DATE: 2003-01-21

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.3

SEQ ID NO 3

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic peptide

US-10-541-343-3

Query Match 100.0%; Score 38; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7

Db 1 WMLSAFS 7

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RESULT 2
US-10-541-343-6
; Sequence 6, Application US/10541343
; Publication No. US2006052299A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond Ming Wah
; TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
; FILE REFERENCE: 2001-103US
; CURRENT APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: PCT/US2004/001468
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,722
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-541-343-6

Query Match      100.0%; Score 38; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
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Db      2 WMLSAFS 8

RESULT 3
US-09-989-481-4
; Sequence 4, Application US/09989481
; Publication No. US20020086831A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-4
; CURRENT APPLICATION NUMBER: US/09/989,481
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 09/633,447
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-989-481-4

Query Match      100.0%; Score 38; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 6; 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
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Db      12 WMLSAFS 18

RESULT 4
US-10-858-545-4
; Sequence 4, Application US/10858545
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; Publication No. US20040224894A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-3
; CURRENT APPLICATION NUMBER: US/10/858,545
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/09/592,018
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-858-545-4

Query Match      100.0%; Score 38; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 6; 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
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Db      12 WMLSAFS 18

RESULT 5
US-10-858-286-4
; Sequence 4, Application US/10858286
; Publication No. US20040242486A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-3
; CURRENT APPLICATION NUMBER: US/10/858,286
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/09/592,018
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-858-286-4

Query Match      100.0%; Score 38; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 6; 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
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Db      12 WMLSAFS 18

RESULT 6
US-10-858-543-4
; Sequence 4, Application US/10858543
; Publication No. US2004026691A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
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; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-3
; CURRENT APPLICATION NUMBER: US/10/858,543
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/09/592,018
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-858-543-4
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Best Local Similarity 100.0%; Pred. No. 6.8;
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QY      1 WMLSAFS 7
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Db      12 WMLSAFS 18
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RESULT 7
US-10-858-144-4
; Sequence 4, Application US/10858144
; Publication No. US20060025565A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M.W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotropic Factors
; FILE REFERENCE: 12592-3
; CURRENT APPLICATION NUMBER: US/10/858,144
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/09/592,018
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 08/9928862
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 08/751225
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/026792
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-858-144-4
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Query Match      100.0%; Score 38; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WMLSAFS 7
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Db      12 WMLSAFS 18
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RESULT 8
US-10-541-343-1
; Sequence 1, Application US/10541343
; Publication No. US20060052299A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond Ming Wah
; APPLICANT: Ko, Pui-Yuk Dorothy
; TITLE OF INVENTION: WMTF Peptides and Compositions and Methods of Use
; FILE REFERENCE: 2001-1030US
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; CURRENT APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: PCT/US2004/001468
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,722
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-541-343-1
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Query Match      100.0%; Score 38; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WMLSAFS 7
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Db      12 WMLSAFS 18
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RESULT 9
US-11-097-143-16893
; Sequence 16893, Application US/11097143
; Publication No. US20050208568A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: C000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16893
; LENGTH: 1760
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-16893
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Query Match      92.1%; Score 35; DB 6; Length 1760;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WMLSAFS 7
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Db      966 WMLSAFS 972
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RESULT 10
US-10-424-599-187845
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Sequence 187845, Application US/10424599
GENERAL INFORMATION: US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 285684
SEQ. ID NO 187845
LENGTH: 103
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_140637C.1.pep
US-10-424-599-187845

Query Match 89.5%; Score 34; DB 4; Length 103;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPS 7
DB 29 WMLGAPS 35

RESULT 11
US-10-124-557-18
Sequence 18, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth C.
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-124-557-18

Query Match 86.8%; Score 33; DB 4; Length 46;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPS 7
DB 5 WMLSPS 11

RESULT 12
US-11-169-232-18
Sequence 18, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-11-169-232-18

Query Match 86.8%; Score 33; DB 6; Length 46;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 5 WMLSPFS 11

RESULT 13

US-09-925-301-1452
Sequence 1452, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1452
LENGTH: 61
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1452

Query Match 86.8%; Score 33; DB 3; Length 61;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 37 WMLSPFS 43

RESULT 14

US-10-124-557-72
Sequence 72, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-124-557-72

Query Match 86.8%; Score 33; DB 4; Length 237;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 111 WMLSPFS 117

RESULT 15

US-11-169-232-72
Sequence 72, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-11-169-232-72

Query Match 86.8%; Score 33; DB 6; Length 237;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 111 WMLSPFS 117

RESULT 16
US-10-124-557-64
Sequence 64, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-124-557-64

Query Match 86.8%; Score 33; DB 4; Length 372;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 139 WMLSPFS 145

RESULT 17
US-11-169-232-64
Sequence 64, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-11-169-232-64

Query Match 86.8%; Score 33; DB 6; Length 372;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 139 WMLSPFS 145

RESULT 18

US-10-124-557-68
; Sequence 68, Application US/10124557
; Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-124-557-68

Query Match 86.8%; Score 33; DB 4; Length 422;
Best Local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 189 WMLSPFS 195

RESULT 19

US-11-169-232-68
; Sequence 68, Application US/11169232
; Publication No. US20060025570A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine

Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-11-169-232-68

Query Match 86.8%; Score 33; DB 6; Length 422;
Best Local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
Db 189 WMLSPFS 195

RESULT 20

US-10-124-557-66
; Sequence 66, Application US/10124557
; Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-124-557-66

Query Match 86.8%; Score 33; DB 4; Length 423;
Best Local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPS 7
DB 190 WMLSPS 196

RESULT 21
US-11-169-232-66
Sequence 66, Application US/11169232
Publication No. US2006025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232

FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-11-169-232-66

Query Match 86.8%; Score 33; DB 6; Length 423;
Best Local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPS 7
DB 190 WMLSPS 196

RESULT 22
US-10-124-557-54
Sequence 54, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-124-557-54

Query Match 86.8%; Score 33; DB 4; Length 463;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 230 WMLSPFS 236

RESULT 23
US-11-169-232-54
Sequence 54, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-11-169-232-54

Query Match 86.8%; Score 33; DB 6; Length 463;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 230 WMLSPFS 236

RESULT 24
US-10-038-694-3
Sequence 3, Application US/10038694
Publication No. US20030180948A1
GENERAL INFORMATION:
APPLICANT: Dixon, Eric
APPLICANT: Hutchins, Jeff T.
APPLICANT: Kuettnier, Klaus E.
APPLICANT: Schmid, Thomas M.
APPLICANT: Schumacher, Barbara L.
APPLICANT: Su, Jui-Ian
TITLE OF INVENTION: SUPERFICIAL ZONE PROTEIN AND METHODS OF
FILE REFERENCE: 07083,000805
CURRENT APPLICATION NUMBER: US/10/038,694
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,920
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 538
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence; note =
US-10-038-694-3

Query Match 86.8%; Score 33; DB 4; Length 538;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 305 WMLSPFS 311

RESULT 25
US-09-802-207-27
Sequence 27, Application US/09802207
Publication No. US20020086824A1
GENERAL INFORMATION:
APPLICANT: Warman, Matthew
APPLICANT: Carpen, John
APPLICANT: Trent, Jeffrey
APPLICANT: Marcelino, Jose
TITLE OF INVENTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
FILE REFERENCE: Case-06212
CURRENT APPLICATION NUMBER: US/09/802,207
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 09/619,175
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,328
PRIOR FILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 792
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: NON CONS
LOCATION: (267)..(268)
NAME/KEY: NON CONS
LOCATION: (321)..(322)
US-09-802-207-27

Query Match 86.8%; Score 33; DB 3; Length 792;
Best Local Similarity 85.7%; Pred. No. 9.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 559 WMLSPFS 565

RESULT 26
US-10-425-115-337015
Sequence 337015, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 337015
LENGTH: 1046
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1046)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_70527C.1.pep
US-10-425-115-337015

Query Match 86.8%; Score 33; DB 4; Length 1046;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 890 WMLSPFS 896

RESULT 27
US-10-124-557-44
Sequence 44, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-10-124-557-44

Query Match 86.8%; Score 33; DB 4; Length 1270;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 1037 WMLSPFS 1043

RESULT 28
US-11-169-232-44
Sequence 44, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232

FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-Jan-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-Jun-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-Dec-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-Aug-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserf, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-11-169-232-44

Query Match 86.8%; Score 33; DB 6; Length 1270;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 1037 WMLSPFS 1043

RESULT 29
US-10-124-557-42
Sequence 42, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Gesner, Rodney M.
Hewick, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-Jan-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-Jun-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-Dec-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-Aug-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserf, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851

APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-Aug-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserf, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42

Query Match 86.8%; Score 33; DB 4; Length 1311;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WMLSAFS 7
Db 1078 WMLSPFS 1084

RESULT 30
US-11-169-232-42
Sequence 42, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Gesner, Rodney M.
Hewick, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-Jan-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-Jun-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-Dec-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-Aug-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserf, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-11-169-232-42

Query Match 86.8%; Score 33; DB 6; Length 1311;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 1078 WMLSPFS 1084

RESULT 31

US-10-124-557-142
Sequence 142, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-124-557-142

Query Match 86.8%; Score 33; DB 4; Length 1313;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
DB 1080 WMLSPFS 1086

RESULT 32

US-11-169-232-142
Sequence 142, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-11-169-232-142

Query Match 86.8%; Score 33; DB 6; Length 1313;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WMLSAFS 7
DB 1080 WMLSPFS 1086

RESULT 33
US-10-124-557-50

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; Sequence 50, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
;               Clark, Stephen C.
;               Jacobs, Kenneth
;               Gesner, Rodney M.
;               Hewick, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; TELECOMMUNICATION INFORMATION:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50

Query Match      86.8%; Score 33; DB 4; Length 1314;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
Db      1081 WMLSPFS 1087

RESULT 34
US-11-169-232-50
; Sequence 50, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
;               Clark, Stephen C.
;               Jacobs, Kenneth
;               Gesner, Rodney M.
;               Hewick, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; TELECOMMUNICATION INFORMATION:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-11-169-232-50
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; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; TELECOMMUNICATION INFORMATION:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-11-169-232-50

Query Match      86.8%; Score 33; DB 6; Length 1314;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAFS 7
Db      1081 WMLSPFS 1087

RESULT 35
US-10-124-557-46
; Sequence 46, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
;               Clark, Stephen C.
;               Jacobs, Kenneth
;               Gesner, Rodney M.
;               Hewick, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-124-557-46

Query Match 86.8%; Score 33; DB 4; Length 1320;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
DB 1087 WMLSPFS 1093

RESULT 36
US-10-124-557-60
Sequence 60, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-124-557-60

Query Match 86.8%; Score 33; DB 4; Length 1320;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
DB 1087 WMLSPFS 1093

RESULT 37
US-10-717-665-58
Sequence 58, Application US/10717665
Publication No. US20050106579A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: IU 103 R1
CURRENT APPLICATION NUMBER: US/10/717,665
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/10/164,595
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
LENGTH: 1320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-717-665-58

Query Match 86.8%; Score 33; DB 5; Length 1320;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
DB 1087 WMLSPFS 1093

RESULT 38
US-11-169-232-46
Sequence 46, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

```

; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-Jan-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-Jun-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
;
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-11-169-232-46

Query Match      86.8%; Score 33; DB 6; Length 1320;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSPFS 7
Db      1087 WMLSPFS 1093

RESULT 39
US-11-169-232-60
; Sequence 60, Application US/11169232
; Publication No. US20060025570A1
;
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.
;
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; FILING DATE: 29-JUN-1990
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-Jan-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-Jun-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
;
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-11-169-232-60

Query Match      86.8%; Score 33; DB 6; Length 1320;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSPFS 7
Db      1087 WMLSPFS 1093

RESULT 40
US-10-124-557-48
; Sequence 48, Application US/10124557
; Publication No. US20020137894A1
;
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.
;
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-Jan-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
```

APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-124-557-48

Query Match 86.8%; Score 33; DB 4; Length 1354;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 1121 WMLSPFS 1127

RESULT 41
US-11-169-232-48
Sequence 48, Application US/11169232
Publication No. US2006002570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-124-557-40

TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-11-169-232-48

Query Match 86.8%; Score 33; DB 6; Length 1354;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSPFS 7
Db 1121 WMLSPFS 1127

RESULT 42
US-10-124-557-40
Sequence 40, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-124-557-40

Query Match 86.8%; Score 33; DB 4; Length 1361;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
Db 1128 WMLSPFS 1134

RESULT 43
US-11-169-232-40
; Sequence 40, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-11-169-232-40

Query Match 86.8%; Score 33; DB 6; Length 1361;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
Db 1128 WMLSPFS 1134

RESULT 44
US-10-124-557-52
; Sequence 52, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.

; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-124-557-52

Query Match 86.8%; Score 33; DB 4; Length 1363;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WMLSAFS 7
Db 1130 WMLSPFS 1136

RESULT 45
US-11-169-232-52
; Sequence 52, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Gesner, Thomas G.

; TITLE OF INVENTION: Megakaryocyte Stimulating Factors

```
;
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Geert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
;
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
;
; US-11-169-232-52
;
; Query Match
; Best Local Similarity 86.8%; Score 33; DB 6; Length 1363;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 WMLSPFS 7
; Db 1130 WMLSPFS 1136
;
; RESULT 46
; US-09-802-207-30
; Sequence 30, Application US/09802207
; Publication No. US20020086824A1
; GENERAL INFORMATION:
; APPLICANT: Warman, Matthew
; APPLICANT: Carpen, John
; APPLICANT: Trent, Jeffrey
; APPLICANT: Marcelino, Jose
; TITLE OF INVENTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
; FILE REFERENCE: Case-06212
; CURRENT APPLICATION NUMBER: US/09/802,207
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 09/619,175
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,328
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
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;
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-802-207-30
;
; Query Match
; Best Local Similarity 86.8%; Score 33; DB 3; Length 1404;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 WMLSPFS 7
; Db 1171 WMLSPFS 1177
;
; RESULT 47
; US-09-897-188-1
; Sequence 1, Application US/09897188
; Publication No. US20040072741A1
; GENERAL INFORMATION:
; APPLICANT: Jay, Gregory D.
; TITLE OF INVENTION: Tribolectin Polypeptides and Uses Thereof
; FILE REFERENCE: 21486-026 CIP2
; CURRENT APPLICATION NUMBER: US/09/897,188
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 09/298,970
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 09/556,246
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-897-188-1
;
; Query Match
; Best Local Similarity 86.8%; Score 33; DB 3; Length 1404;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 WMLSPFS 7
; Db 1171 WMLSPFS 1177
;
; RESULT 48
; US-10-124-557-2
; Sequence 2, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; APPLICANT: Clark, Stephen C.
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Geener, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-124-557-2

Query Match 86.8%; Score 33; DB 4; Length 1404;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

RESULT 49

US-10-124-557-62
Sequence 62, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:

APPLICANT: Turner, Katherine

Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann

REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-124-557-62

Query Match 86.8%; Score 33; DB 4; Length 1404;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

RESULT 50

US-10-858-595-1
Sequence 1, Application US/10858595
Publication No. US20040229804A1
GENERAL INFORMATION:

APPLICANT: Jay, Gregory D.
TITLE OF INVENTION: TRIBONECTINS
FILE REFERENCE: 21486-026
CURRENT APPLICATION NUMBER: US/10/858,595
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US/09/298,970
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1404
TYPE: PRT
ORGANISM: Homo sapiens
US-10-858-595-1

Query Match 86.8%; Score 33; DB 5; Length 1404;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 1171 WMLSPFS 1177

Search completed: August 29, 2006, 10:18:50
Job time : 87.6931 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model1

Run on: August 29, 2006, 09:43:08 ; Search time 5.54455 Seconds
(without alignments)
86.383 Million cell updates/sec

Title: US-10-541-343-3

Perfect score: 38

Sequence: 1 WMLSAFS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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2	31	81.6	302	US-10-449-902-38264	Sequence 38264, A
3	31	81.6	302	US-11-174-307B-5396	Sequence 5396, Ap
4	31	81.6	371	US-11-399-675-14	Sequence 14, Appl
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461	25	65.8	543	7	US-11-190-750-78	Sequence 78, Appl							
462	25	65.8	543	7	US-11-264-784-79	Sequence 79, Appl							
463	25	65.8	543	7	US-11-264-737-120	Sequence 120, Appl							

RESULT 1
US-10-449-902-28641
; Sequence 28641, Application US/10449902
; Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute for Physical and Chemical Research.
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
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NUMBER OF SEQ ID NOS: 56791
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SEQ ID NO 28641
LENGTH: 301
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-28641

Query Match 81.6%; Score 31; DB 6; Length 301;
Best Local Similarity 71.4%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2

US-10-449-902-38264
; Sequence 38264, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38264
; LENGTH: 302
; TYPE: PRT
; ORGANISM: *Oryza sativa*
US-10-449-902-38264

Query Match 81.6%; Score 31; DB 6; Length 302;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLTVFS 7
Db 193 WMLTVFS 199

RESULT 3

US-11-174-307B-5396
; Sequence 5396, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
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; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 5396
; LENGTH: 302
; TYPE: PRT
; ORGANISM: *Zea mays*
US-11-174-307B-5396

Query Match 81.6%; Score 31; DB 7; Length 302;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLTVFS 7
Db 193 WMLTVFS 199

RESULT 4
US-11-399-675-14

; Sequence 14, Application US/11399675
; Publication No. US20060179513A1
; GENERAL INFORMATION:
; APPLICANT: Sticklen, Masomeh B
; APPLICANT: Magbool, Shahina B
; APPLICANT: Dale, Bruce E
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULOSE WHICH
; FILE REFERENCE: MSU 4.1-814
; CURRENT APPLICATION NUMBER: US/11/399,675
; CURRENT FILING DATE: 2006-04-06
; PRIOR APPLICATION NUMBER: US 60/242,408
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/981,900
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14
; LENGTH: 371
; TYPE: PRT
; ORGANISM: *Phanerochaete chrysosporium*
US-11-399-675-14

Query Match 81.6%; Score 31; DB 7; Length 371;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLTVFS 7
Db 197 WMLTVFS 203

RESULT 5
US-11-353-390A-14
; Sequence 14, Application US/11353390A
; Publication No. US20060185036A1
; GENERAL INFORMATION:
; APPLICANT: Sticklen, Masomeh B
; APPLICANT: Magbool, Shahina B
; APPLICANT: Dale, Bruce E
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULOSE WHICH
; FILE REFERENCE: MSU 4.1-806
; CURRENT APPLICATION NUMBER: US/11/353,390A
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: US 60/242,408
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/981,900
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14
; LENGTH: 371
; TYPE: PRT
; ORGANISM: *Phanerochaete chrysosporium*
US-11-353-390A-14

Query Match 81.6%; Score 31; DB 7; Length 371;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLTVFS 7
Db 197 WMLTVFS 203

RESULT 6
US-11-354-310A-14
; Sequence 14, Application US/11354310A
; Publication No. US20060185037A1
; GENERAL INFORMATION:
; APPLICANT: Sticklen, Masomeh B
; APPLICANT: Magbool, Shahina B

```

; APPLICANT: Dale, Bruce E
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
; FILE REFERENCE: DEGRADE LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS
; CURRENT FILING DATE: 2006-02-14/354,310A
; PRIOR APPLICATION NUMBER: US 60/242,408
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/981,900
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Phanerochaete chrysosporium
US-11-354-310A-14

Query Match      81.6%; Score 31; DB 7; Length 371;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
Db      197 WMLSAHS 203
```

```

RESULT 7
US-10-449-902-52867
; Sequence 52867, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 52867
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52867

Query Match      78.9%; Score 30; DB 6; Length 504;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
Db      213 WMLRAFT 219
```

```

RESULT 8
US-10-449-902-46155
; Sequence 46155, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
```

```

; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46155
; LENGTH: 1128
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46155

Query Match      78.9%; Score 30; DB 6; Length 1128;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
Db      451 WMLSLFN 457
```

```

RESULT 9
US-10-449-902-53284
; Sequence 53284, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53284
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53284

Query Match      76.3%; Score 29; DB 6; Length 63;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
Db      22 WMLVAFA 28
```

```

RESULT 10
US-10-449-902-44647
; Sequence 44647, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
```

NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44647
LENGTH: 95
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-44647

Query Match 76.3%; Score 29; DB 6; Length 95;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 54 WMLAAFA 60

RESULT 11
US-11-056-355B-79384
Sequence 79384, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 79384
LENGTH: 297
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(297)
OTHER INFORMATION: Ceres Seq. ID no. 12651075
US-11-056-355B-79384

Query Match 76.3%; Score 29; DB 7; Length 297;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 219 WMLIAFS 225

RESULT 12
US-10-953-38417
Sequence 38417, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38417
LENGTH: 308
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-38417

Query Match 76.3%; Score 29; DB 6; Length 308;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 233 WMLIAFS 239

RESULT 13
US-11-056-355B-79383
Sequence 79383, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 79383
LENGTH: 308
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(308)
OTHER INFORMATION: Ceres Seq. ID no. 12651074
US-11-056-355B-79383

Query Match 76.3%; Score 29; DB 7; Length 308;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 230 WMLIAFS 236

RESULT 14
US-11-056-355B-82525
Sequence 82525, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 82525
LENGTH: 334
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(334)
OTHER INFORMATION: Ceres Seq. ID no. 12660048
US-11-056-355B-82525

Query Match 76.3%; Score 29; DB 7; Length 334;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
DB 306 WMLAAFT 312


```
RESULT 15
US-10-511-455-26
; Sequence 26, Application US/10511455
; Publication No. US2006008835A1
; GENERAL INFORMATION:
; APPLICANT: Pickard, Benjamin Simon
; APPLICANT: Blackwood, Douglas
; APPLICANT: Porteous, David
; APPLICANT: Muir, Walter John
; APPLICANT: Mors, Ole
; APPLICANT: Ewald, Henrik Lykke
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511.455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-26

Query Match      76.3%; Score 29; DB 6; Length 335;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 WMLSAF 6
      |||||
Db      316 WMLSIF 321

RESULT 16
US-11-395-249-4
; Sequence 4, Application US/11395249
; Publication No. US20060177904A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Werberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000103.6
; CURRENT APPLICATION NUMBER: US/11/395,249
; CURRENT FILING DATE: 2006-04-03
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-11-395-249-4

Query Match      76.3%; Score 29; DB 7; Length 335;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 WMLSAF 6
      |||||
Db      316 WMLSIF 321

RESULT 17
US-11-056-355B-82529
; Sequence 82529, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82529
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(338)
; OTHER INFORMATION: Cereas Seq. ID no. 1266052
US-11-056-355B-82529

Query Match      76.3%; Score 29; DB 7; Length 338;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 WMLSAFS 7
      |||||
Db      310 WMLNAFT 316

RESULT 18
US-10-953-349-33299
; Sequence 33299, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33299
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33299

Query Match      76.3%; Score 29; DB 6; Length 345;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 WMLSAFS 7
      |||||
Db      270 WMLIAFS 276
```


RESULT 19
US-10-953-349-38416
; Sequence 38416, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38416
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38416

Query Match 76.3%; Score 29; DB 6; Length 345;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 270 WMLIAFS 276

RESULT 20
US-11-056-355B-79382
; Sequence 79382, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 79382
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(351)
; OTHER INFORMATION: Ceres Seq. ID no. 12651073
US-11-056-355B-79382

Query Match 76.3%; Score 29; DB 7; Length 351;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 273 WMLIAFS 279

RESULT 21
US-10-449-902-30511
; Sequence 30511, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30511
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30511

Query Match 76.3%; Score 29; DB 6; Length 354;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 279 WMLIAFS 285

RESULT 22
US-10-449-902-49957
; Sequence 49957, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49957
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49957

Query Match 76.3%; Score 29; DB 6; Length 354;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
Db 279 WMLIAFS 285

RESULT 23
US-10-953-349-32815
; Sequence 32815, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32815
; LENGTH: 355
; TYPE: PRT

; ORGANISM: Zea mays subsp. mays
US-10-953-349-32815

Query Match 76.3%; Score 29; DB 6; Length 355;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
|:|
Db 280 WMLTAFS 286

RESULT 24
US-11-056-355B-11231
; Sequence 11231, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 11231
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(355)
; OTHER INFORMATION: Ceres Seq. ID no. 13492044
US-11-056-355B-11231

Query Match 76.3%; Score 29; DB 7; Length 355;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
|:|
Db 280 WMLTAFS 286

RESULT 25
US-11-056-355B-17746
; Sequence 17746, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17746
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(355)
; OTHER INFORMATION: Ceres Seq. ID no. 13492044
US-11-056-355B-17746

Query Match 76.3%; Score 29; DB 7; Length 355;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
|:|
Db 280 WMLTAFS 286

RESULT 26
US-10-953-349-33298
; Sequence 33298, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33298
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33298

Query Match 76.3%; Score 29; DB 6; Length 357;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
|:|
Db 282 WMLTAFS 288

RESULT 27
US-10-953-349-38415

; Sequence 38415, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38415
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38415

Query Match 76.3%; Score 29; DB 6; Length 357;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMLSAFS 7
|:|
Db 282 WMLTAFS 288

RESULT 28
US-11-330-403-6594

; Sequence 6594, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330.403
; CURRENT FILING DATE: 2006-01-12

NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 6594
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15
US-11-330-403-6594

Query Match 76.3%; Score 29; DB 7; Length 367;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAF 6
|:|:|:|
Db 43 WMLSLF 48

RESULT 29
US-10-449-902-38671
; Sequence 38671, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020571-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38671
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38671

Query Match 76.3%; Score 29; DB 6; Length 388;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:|
Db 311 WMLIAFS 317

RESULT 30
US-10-953-349-33297
; Sequence 33297, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33297
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33297

Query Match 76.3%; Score 29; DB 6; Length 417;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:|
Db 342 WMLIAFS 348

RESULT 31
US-10-953-349-32813
; Sequence 32813, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32813
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-32813

Query Match 76.3%; Score 29; DB 6; Length 418;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:|
Db 343 WMLIAFS 349

RESULT 32
US-11-056-355B-11229
; Sequence 11229, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 11966
; SEQ ID NO 11229
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)-(418)
; OTHER INFORMATION: Ceres Seq. ID no. 13492042
US-11-056-355B-11229

Query Match 76.3%; Score 29; DB 7; Length 418;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:|
Db 343 WMLIAFS 349

RESULT 33
US-11-056-355B-17744
; Sequence 17744, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav

```

; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17744
; LENGTH: 418
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(418)
; OTHER INFORMATION: Ceres Seq. ID no. 13492042
US-11-056-355B-17744

```

```

Query Match      76.3%; Score 29; DB 7; Length 418;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 WMLSAFS 7
Db      343 WMLAFT 349

```

```

RESULT 34
US-11-056-355B-82524
; Sequence 82524, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82524
; LENGTH: 437
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(437)
; OTHER INFORMATION: Ceres Seq. ID no. 12666047
US-11-056-355B-82524

```

```

Query Match      76.3%; Score 29; DB 7; Length 437;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 WMLSAFS 7
Db      409 WMLAFT 415

```

```

RESULT 35
US-11-056-355B-82528
; Sequence 82528, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B

```

```

; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82528
; LENGTH: 438
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(438)
; OTHER INFORMATION: Ceres Seq. ID no. 12666051
US-11-056-355B-82528

```

```

Query Match      76.3%; Score 29; DB 7; Length 438;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 WMLSAFS 7
Db      410 WMLAFT 416

```

```

RESULT 36
US-10-953-349-31757
; Sequence 31757, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31757
; LENGTH: 495
; TYPE: prt
; ORGANISM: Trifolium aestivum
US-10-953-349-31757

```

```

Query Match      76.3%; Score 29; DB 6; Length 495;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 WMLSAFS 7
Db      60 WMLAFT 66

```

```

RESULT 37
US-11-056-355B-66755
; Sequence 66755, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 66755
; LENGTH: 495
; TYPE: prt
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(495)

```

OTHER INFORMATION: Ceres Seq. ID no. 14302422
US-11-056-355B-66755

Query Match 76.3%; Score 29; DB 7; Length 495;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:
Db 60 WALAASF 66

RESULT 38
US-10-953-349-31756

; Sequence 31756, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31756
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31756

Query Match 76.3%; Score 29; DB 6; Length 530;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:
Db 95 WALAASF 101

RESULT 39
US-11-056-355B-66754

; Sequence 66754, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 66754
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(530)
; OTHER INFORMATION: Ceres Seq. ID no. 14302421
US-11-056-355B-66754

Query Match 76.3%; Score 29; DB 7; Length 530;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:
Db 95 WALAASF 101

RESULT 40
US-11-056-355B-82523

; Sequence 82523, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82523
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(564)
; OTHER INFORMATION: Ceres Seq. ID no. 1266046
US-11-056-355B-82523

Query Match 76.3%; Score 29; DB 7; Length 564;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:
Db 536 WMLAAPT 542

RESULT 41
US-11-056-355B-82527

; Sequence 82527, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82527
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(565)
; OTHER INFORMATION: Ceres Seq. ID no. 1266050
US-11-056-355B-82527

Query Match 76.3%; Score 29; DB 7; Length 565;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMLSAFS 7
|:|:|:
Db 537 WMLAAPT 543

RESULT 42
US-10-449-902-47030
; Sequence 47030, Application US/10449902
; Publication No. US20060123505A1

```
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47030
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-47030
```

```
Query Match          76.3%; Score 29; DB 6; Length 599;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
        |||
Db      168 WALAAPS 174
```

```
RESULT 43
; Sequence 31755, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31755
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-31755
```

```
Query Match          76.3%; Score 29; DB 6; Length 610;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
        |||
Db      175 WALAAPS 181
```

```
RESULT 44
; Sequence 66753, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
```

```
; SEQ ID NO 66753
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(610)
; OTHER INFORMATION: Ceres Seq. ID no. 14302420
; US-11-056-355B-66753
```

```
Query Match          76.3%; Score 29; DB 7; Length 610;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAFS 7
        |||
Db      175 WALAAPS 181
```

```
RESULT 45
; Sequence 33831, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33831
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; US-10-953-349-33831
```

```
Query Match          76.3%; Score 29; DB 6; Length 638;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAF 6
        |||
Db      483 WMLSRF 488
```

```
RESULT 46
; Sequence 33830, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33830
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; US-10-953-349-33830
```

```
Query Match          76.3%; Score 29; DB 6; Length 665;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WMLSAF 6
        |||
Db      510 WMLSRF 515
```

```
RESULT 47
US-10-953-349-33829
; Sequence 33829, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33829
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33829

Query Match      76.3%; Score 29; DB 6; Length 667;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WMLSAF 6
Db      512 WMLSRF 517

RESULT 48
US-11-056-355B-1496
; Sequence 1496, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 1496
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(105)
; OTHER INFORMATION: Ceres Seq. ID no. 12411161
US-11-056-355B-1496

Query Match      73.7%; Score 28; DB 7; Length 105;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAF 6
Db      100 WMLAAF 105

RESULT 49
US-11-056-355B-1495
; Sequence 1495, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 1495
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(124)
; OTHER INFORMATION: Ceres Seq. ID no. 12411160
US-11-056-355B-1495

Query Match      73.7%; Score 28; DB 7; Length 124;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAF 6
Db      119 WMLAAF 124

RESULT 50
US-11-056-355B-1494
; Sequence 1494, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 1494
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(154)
; OTHER INFORMATION: Ceres Seq. ID no. 12411159
US-11-056-355B-1494

Query Match      73.7%; Score 28; DB 7; Length 154;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WMLSAF 6
Db      149 WMLAAF 154

Search completed: August 29, 2006, 11:29:12
Job time : 5.54455 secs
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